Run on:

sequence: ritle: perfect score:

Scoring table:

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Page 1
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OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 2000000000
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   published_Applications_NA:*

| cgn2_6/ptodata/1/pubpna/P
| cgn2_6/ptodata/1/pubpna/P
| cgn2_6/ptodata/1/pubpna/P
| cgn2_6/ptodata/1/pubpna/U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1660708 seqs, 1229959015 residues
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Copyright (c) 1993 - 2003 Compugen Ltd.
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1: /cgn2_6/ptodata/I/pubpna/US07_NEW_PUB.seq:*
2: /cgn2_6/ptodata/I/pubpna/US06_NEW_PUB.seq:*
3: /cgn2_6/ptodata/I/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/I/pubpna/US07_NEW_PUB.seq:*
5: /cgn2_6/ptodata/I/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/I/pubpna/US07_NEW_PUB.seq:*
7: /cgn2_6/ptodata/I/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/I/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/I/pubpna/US08_PUBCOMB.seq:*
10: /cgn2_6/ptodata/I/pubpna/US09_PUBCOMB.seq:*
11: /cgn2_6/ptodata/I/pubpna/US09_NEW_PUB.seq:*
11: /cgn2_6/ptodata/I/pubpna/US108_PUBCOMB.seq:*
12: /cgn2_6/ptodata/I/pubpna/US108_PUBCOMB.seq:*
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14: /cgn2_6/ptodata/I/pubpna/US108_PUBCOMB.seq:*
15: /cgn2_6/ptodata/I/pubpna/US10_NEW_PUB.seq:*
16: /cgn2_6/ptodata/I/pubpna/US10_NEW_PUB.seq:*
17: /cgn2_6/ptodata/I/pubpna/US10_NEW_PUB.seq:*
18: /cgn2_6/ptodata/I/pubpna/US10_NEW_PUB.seq:*
19: /cgn2_6/ptodata/I/pubpna/US10_NEW_PUB.seq:*
10: /cgn2_6/ptodata/I/pubpna/US10_NEW_PUB.seq:*
11: /cgn2_6/ptodata/I/pubpna/US10_NEW_PUB.seq:*
12: /cgn2_6/ptodata/I/pubpna/US10_NEW_PUB.seq:*
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547
533
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   3 US-10-081-817-19
2 US-10-059-579-120
2 US-10-059-579-120
2 US-10-27-632-196114
3 US-10-237-435-6
4 US-10-210-951-27
12 US-10-951-27
12 US-09-989-723-407
12 US-09-989-723-407
13 US-09-989-737-407
14 US-09-989-737-407
15 US-09-980-731-407
16 US-09-991-073-407
17 US-09-991-073-407
18 US-09-991-073-407
19 US-09-991-073-407
10 US-09-991-163-407
10 US-09-991-163-407
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10 US-09-991-163-407
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                        Sequence 19, Appl Sequence 126114, Sequence 196114, Sequence 67, Appli Sequence 407, App Sequence 407, App
                                                                                                                                                                                                                                                                                                                                                                                                                                               Description
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Sequence 19, Application US/10081817

Sequence 19, Application US/10081817

Publication No. US20020183501A1

GENERAL INFORMATION: Kornelia

APPLICANT: POLYAK, Kornelia

APPLICANT: POLYET, Dale

APPLICANT: SGTCAI, Dale

APPLICANT: KTOP, Ian

FILE REFERENCE: 100830-094001

FILE REFERENCE: 100830-094001

FILE REFERENCE: 100830-094001

CURRENT APPLICATION UNMBER: 05/10/081/817

CURRENT APPLICATION UNMBER: 60/270,973

PRIOR APPLICATION UNMBER: 60/270,973

PRIOR APPLICATION UNMBER: 60/351,908

PRIOR APPLICATION UNMBER: 00/351,908

PRIOR FILING DATE: 2002-01-25

PRIOR FILING DATE: 2002-01-25

PRIOR FILING DATE: 2002-01-25

PRIOR FILING DATE: 2002-01-25

PRIOR FILING DATE: 32

UNMBER OF SEQ ID NOS: 32

UNMBER OF SEQ ID NOS: 32

LENGTH: 547

TYPEF: DNA
                                                                                                                                                                                                                                                                                                                           TYPE: DAN
TYPE: DAN
ORGANISM: Homo saplens
PEATURE:
PEATURE:
LOCATION: 186
LOCATION: 187
OTHER INFORMATION: n = C
US-10-081-817-19
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US-10-081-817-19
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                                                                                                                                                                                                                                Query Match 92.4
Query Match Similarity 97.8
Best Local Similarity 97.8
Matches 539; Conservative
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                                                                                                                                     92.4%;
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US-09-989-738-407
US-09-989-735-407
US-09-989-735-407
US-09-989-730-407
US-09-991-181-407
US-09-991-48-407
US-09-991-687-407
US-09-991-687-407
US-09-997-653-407
US-09-997-653-407
US-09-997-666-407
US-09-997-666-407
US-09-991-181-407
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Result

Score

Match

120

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429

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                                                                                                                                                             NAME/KEY: misc_feature; LOCATION: (359)..(359); OTHER INFORMATION: n is US-10-059-579-120
                                                                                                                                                                                                                                                                                                                                    APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF I
APPLICANT: SUKUMAR, SATASWALI
APPLICANT: EVGON, Ella
APPLICANT: DOOLEY, William C.
APPLICANT: DAVIDSON, NANCY
APPLICANT: FACKLER, MALY JO.
TITLE OF INVENTION: ABBERRANTLY METHYLATED GENES AS
FILE REFERENCE: JHU1630-1
CURRENT APPLICATION NUMBER: US/10/059,579
CURRENT FILING DATE: 2003-02-03
PRIOR APPLICATION NUMBER: US 09/771,357
PRIOR APPLICATION NUMBER: US 09/771,357
PRIOR FILING DATE: 2011-126
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                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn version
SEQ ID NO 120
LENGTH: 1794
                                                                                                              Query Match
Best Local
                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 120,
                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 136
                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          541
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   190 GAGGGAAGCTCCCCTCACCCGGCCCAGCCCTGCAGGGGGGGCGCGTGGGGGTCAGACCGCAA
                                                                                                              Similarity
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                                  GAGGGAAGCTCCCCTCACCCGGCCCAGCCCTGACGGGGGGGCGC--TGGGGTCAGACCGCAA
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o. US20030138783A1
                                                                                                Conservative
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                                                                                              Score 338.4;
Pred. No. 1.3e
0; Mismatches
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1.3e-64;
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                                                                                                                                                                                                                                                                                                                                                                                                Sequence 196114/c

Sequence 196114, Application US/10027632

GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/193,63
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-08-09
NUMBER OF SECTION NUMBER: US 60/146,002
                                                                                                                                                                                                                                                                                       ; LENGTH: 533
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-196114
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SOFTWARE: FastSEQ for
SEQ ID NO 196114
                                                                                                                                                                                                                             Matches
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Best Local (
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                                                                                                                                                                            1 CGGCCGGGGAGCCGGCCGGGATGAGGCCTGATCGTCCCTGGCGCCTCCACCTCCCCAGG
                                                                                                                                                                                                                                            Similarity
                                                                                                                CGCAGAAGGCGCCCACGAGGACCCCCAGTGCCCGACGTTGCCACGGTCTGGGATCAGAGG
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                                                                                                                                                             CGGCCGGGAGGCGGCGGGAGTGAGGCCTGATCGTCCCTGGCGCCTCCACCTCCCCAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCCCTCACCNG
                                                              CGCAGAAGGCGCCCACGAGGACCCCCAGTGCCCGACGTTGCCACGGTCTGGGATCAGAGG
                                  CACGGGACCAGGGAGCCAGGAACTGCGCCGCCC - - - CGCCCTGCCTGGCGCGA - GGAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGGGCCCCAGCGCCTGCCAAGAGGAAGTCCTCGAGGCCCGGGCAGGGAAGGGGGCACGGG
                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                           26.1%;
   190
                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                          Score 143.6; DB 13
Pred. No. 1.5e-22;
0; Mismatches 5;
                                                                                                                                                                                                                                                           DB 13;
                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                          Length 533
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RESULT 4
US-10-237-435-6
US-10-237-4
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APPLICANT: Stone, Donna M.

APPLICANT: Watanabe, Colin K.

APPLICANT: Wood, William I.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF TUMOR TITLE OF THE P2931R1C1

FILE REFERENCE: P2931R1C1

CURRENT FILING DATE: 1020-08-02

CURRENT FILING DATE: 1996-04-01

PRIOR APPLICATION NUMBER: 60/014699

PRIOR APPLICATION NUMBER: 60/026943

PRIOR APPLICATION NUMBER: 60/026943

PRIOR APPLICATION NUMBER: 60/059352

PRIOR APPLICATION NUMBER: 60/059352

PRIOR FILING DATE: 1997-09-19

PRIOR FILING DATE: 1997-09-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 5
US-10-210-951-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 27, Application US/10210951 Publication No. US20030170228A1
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Godowski, Paul J.
Gurney, Austin L.
Hillan, Kenneth J.
Marsters, Scot A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pitti,Robert M.
Roy,Margaret Ann
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PRIOR FILING DATE: 1997-10-10

PRIOR APPLICATION NUMBER: 60/063755

PRIOR APPLICATION NUMBER: 60/063045

PRIOR APPLICATION NUMBER: 60/063045

PRIOR FILING DATE: 1997-10-24

PRIOR FILING DATE: 1997-10-24

PRIOR PRICATION NUMBER: 60/066511

PRIOR APPLICATION NUMBER: 60/066511

PRIOR PRILING DATE: 1997-11-24

PRIOR FILING DATE: 1997-11-24

PRIOR PRIOR DATE: 1997-11-24

PRIOR APPLICATION NUMBER: 60/066772

PRIOR APPLICATI
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; ORGANISM: Homo sapiens
US-10-210-951-27
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APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Watliams, Indickey
APPLICANT: William I.
APPLICANT: Walliams, Indickey
APPLICANT: Wood, William I.
APPLICANTON UNMER: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION NUMBER: 00/049787
CURRENT APPLICATION NUMBER: 60/049787
PRIOR APPLICATION NUMBER: 60/062250
PRIOR APPLICATION NUMBER: 60/065186
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-10-12
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/065311
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US-09-989-722-407
US-09-989-722-407, A
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Similarity 100.0%;
78; Conservative (
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Botstein, David
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Eaton, Dan L.
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Gerber, Hanspeter
Gerritsen, Mary E.
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Godowski, Paul J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Grimaldi, J. Christopher
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Kljavin, Ivar J.
Napier, Mary A.
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, pred. No. 1.9e-08;
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FILING DATE: 1997-11-13
APPLICATION NUMBER: 60/066770
FILING DATE: 1997-11-24
APPLICATION NUMBER: 60/075945
FILING DATE: 1998-02-25

APPLICATION NUMBER: 60/078910 FILING DATE: 1998-03-20

RIOR APPLICATION NUMBER: 60/08 RIOR FILLING DATE: 1998-06-17 RIOR APPLICATION NUMBER: 60/08 RIOR APPLICATION NUMBER: 60/08 RIOR APPLICATION NUMBER: 60/08 RIOR APPLICATION NUMBER: 60/08 RIOR FILLING DATE: 1998-06-17 RIOR APPLICATION NUMBER: 60/08 RIOR FILLING DATE: 1998-06-17 RIOR APPLICATION NUMBER: 60/08 RIOR FILLING DATE: 1998-06-18 RIOR APPLICATION NUMBER: 60/08 RIOR FILLING DATE: 1998-06-18 RIOR APPLICATION NUMBER: 60/08 RIOR FILLING DATE: 1998-06-18 RIOR APPLICATION NUMBER: 60/08 RIOR FILLING DATE: 1998-06-19 RIOR APPLICATION NUMBER: 60/08 RIOR FILLING DATE: 1998-06-19 RIOR APPLICATION NUMBER: 60/08 RIOR FILLING DATE: 1998-06-29 RIOR APPLICATION NUMBER: 60/08 RIOR FILLING DATE: 1998-06-29 RIOR APPLICATION NUMBER: 60/08 RIOR FILLING DATE: 1998-06-22 RIOR APPLICATION NUMBER: 60/08 RIOR FILLING DATE: 1998-06-22 RIOR APPLICATION NUMBER: 60/08 RIOR FILLING DATE: 1998-06-24 RIOR APPLICATION NUMBER: 60/08 RIOR FILLING DATE: 1998-06-25 R				
** APPLICATION NUMBER: 60/08 APPLICATION NUM				
DATE: 1998-06-19 TATION NUMBER: 60/08 DATE: 1998-06-17 VION NUMBER: 60/08 DATE: 1998-06-18 VION NUMBER: 60/08 DATE: 1998-06-18 VION NUMBER: 60/08 DATE: 1998-06-19 VION NUMBER: 60/08 DATE: 1998-06-19 VION NUMBER: 60/08 DATE: 1998-06-19 VION NUMBER: 60/08 DATE: 1998-06-29 VION NUMBER: 60/08 DATE: 1998-06-29 VION NUMBER: 60/08 DATE: 1998-06-24 VION NUMBER: 60/08 DATE: 1998-06-25	**************************************	PRIOR	PRIOR	*
NUMBER: 60/08 1998-06-17 NUMBER: 60/08 1998-06-17 NUMBER: 60/08 1998-06-17 NUMBER: 60/08 1998-06-18 NUMBER: 60/08 1998-06-18 NUMBER: 60/08 1998-06-18 NUMBER: 60/08 1998-06-18 NUMBER: 60/08 1998-06-19 NUMBER: 60/08 1998-06-28 NUMBER: 60/08 1998-06-24 NUMBER: 60/08 1998-06-24 NUMBER: 60/08 1998-06-24 NUMBER: 60/08 1998-06-24 NUMBER: 60/08 1998-06-25 NUMBER: 60/08 1998-06-24 NUMBER: 60/08 1998-06-25	LICATION	NICATION DATE DA	PATES TATION TAT	PPLICATION ILING DATE ILING DATE PPLICATION ILING DATE PPLICATION ILING DATE PPLICATION ILING DATE
-4-3 8 8 6 6 6 6 6 6 6 5 5 5 5 5 4 4 4 4 4 4 4 4	NUMBER: 60/09C 1998-06-25 1998-06-25 1998-06-25 1998-06-26 1998-06-26 1998-06-26 1998-06-26 1998-06-26 1998-06-26 1998-06-26 1998-06-26	1998-06-24 NUMBER: 60/0 NUMBER: 60/0 NUMBER: 60/0 1998-06-24 NUMBER: 60/0 NUMBER: 60/0 1998-06-25 NUMBER: 60/0 1998-06-26 NUMBER: 60/0 1998-06-26 NUMBER: 60/0 1998-06-26 NUMBER: 60/0 1998-06-25 NUMBER: 60/0	1998-06-17 NUMBER: 60/089 1998-06-18 1998-06-18 NUMBER: 60/089 1998-06-18 NUMBER: 60/089 1998-06-19 1998-06-19 NUMBER: 60/089 1998-06-19 NUMBER: 60/089 1998-06-22 NUMBER: 60/090 1998-06-22 NUMBER: 60/090 1998-06-22 NUMBER: 60/090 1998-06-22 NUMBER: 60/090 1998-06-23 NUMBER: 60/090 1998-06-23 NUMBER: 60/090 1998-06-23 NUMBER: 60/090 1998-06-23 NUMBER: 60/090	NUMBER: 60/089 1998-06-17 NUMBER: 60/089 1998-06-17 NUMBER: 60/089 1998-06-17 NUMBER: 60/089 1998-06-17 NUMBER: 60/089

PRIOR PRIOR

APPLICATION NUMBER: 60/088734 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088738

OR FILING DATE: 1998-06-10
OR APPLICATION NUMBER: 60/088742
OR FILING DATE: 1998-06-10
OR APPLICATION NUMBER: 60/088810
OR FILING DATE: 1998-06-10
OR APPLICATION NUMBER: 60/088824
OR FILING DATE: 1998-06-10
OR APPLICATION NUMBER: 60/088826
OR FILING DATE: 1998-06-10
OR APPLICATION NUMBER: 60/088858
OR FILING DATE: 1998-06-11
OR APPLICATION NUMBER: 60/088861
OR FILING DATE: 1998-06-11
OR APPLICATION NUMBER: 60/088861
OR FILING DATE: 1998-06-11
OR APPLICATION NUMBER: 60/088876

PRIOR

OR APPLICATION NUMBER: 60/089105
OR FILING DATE: 1998-06-12
OR APPLICATION NUMBER: 60/089440
OR FILING DATE: 1998-06-16
OR APPLICATION NUMBER: 60/089512
OR FILING DATE: 1998-06-16
OR APPLICATION NUMBER: 60/089514
OR FILING DATE: 1998-06-16

PRIOR PRIOR PRIOR

OR APPLICATION NUMBER: 60/088033
OR FILING DATE: 1998-06-04
OR APPLICATION NUMBER: 60/08826
OR FILING DATE: 1998-06-04
OR APPLICATION NUMBER: 60/088167
OR FILING DATE: 1998-06-05
OR APPLICATION NUMBER: 60/088202
OR FILING DATE: 1998-06-05
OR APPLICATION NUMBER: 60/088212
OR FILING DATE: 1998-06-05
OR APPLICATION NUMBER: 60/088217
OR FILING DATE: 1998-06-05
OR APPLICATION NUMBER: 60/088217
OR APPLICATION NUMBER: 60/088217
OR APPLICATION NUMBER: 60/088217
OR APPLICATION NUMBER: 60/088655
OR APPLICATION NUMBER: 60/088655
OR FILING DATE: 1998-06-09

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OR APPLICATION NUMBER: 60/088025
OR FILING DATE: 1998-06-04
OR APPLICATION NUMBER: 60/088026
OR FILING DATE: 1998-06-04
OR APPLICATION NUMBER: 60/088028
OR FILING DATE: 1998-06-04
OR FILING DATE: 1998-06-04
OR APPLICATION NUMBER: 60/088029
OR FILING DATE: 1998-06-04
OR APPLICATION NUMBER: 60/088030
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OR FILING DATE: 1998-06-02
OR FILING DATE: 1998-06-03
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PRIOR PRIOR PRIOR PRIOR PRIOR

OR APPLICATION NUMBER: 60/083322
OR FILLING DATE: 1998-04-28
OR APPLICATION NUMBER: 60/084600
OR FILLING DATE: 1998-05-07
OR APPLICATION NUMBER: 60/087106
OR FILLING DATE: 1998-05-28
OR FILLING DATE: 1998-05-28

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APPLICANT: FOR MATYS...

APPLICANT: Stewart, Timothy A. APPLICANT: Stewart, Timothy A. APPLICANT: Stewart, Timothy A. APPLICANT: Munas, Daniel APPLICANT: Watanabe, Colin K. APPLICANT: Watanabe, Colin K. APPLICANT: Wood, Williams, P. Mickey APPLICANT: Zhang, Zemin I. APPLICANT: Zhang, Zemin I. APPLICATION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic COURCENT FILING DATE: 2001-11-19

CURRENT APPLICATION NUMBER: 60/09/989,723

CURRENT APPLICATION NUMBER: 60/09/987

PRIOR APPLICATION NUMBER: 60/062250

PRIOR APPLICATION NUMBER: 60/065186

PRIOR APPLICATION NUMBER: 1997-11-12

PRIOR PRILING DATE: 1997-11-12

PRIOR PRILING DATE: 1997-11-13

PRIOR FILING DATE: 1997-11-24
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PRIOR APPLICATION NUMBER: 60/091544
PRIOR APPLICATION UNMEER: 60/091519
PRIOR PRILING DATE: 1998-07-02
PRIOR PPLICATION UNMEER: 60/091626
PRIOR PILING DATE: 1998-07-02
PRIOR PPLICATION UNMEER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION UNMEER: 60/091978
PRIOR APPLICATION NUMBER: 60/091978
PRIOR APPLICATION UNMEER: 60/091982
PRIOR APPLICATION UNMEER: 60/091982
PRIOR APPLICATION UNMEER: 60/091982
PRIOR APPLICATION UNMEER: 60/091982
PRIOR APPLICATION UNMEER: 60/09182
PRIOR APPLICATION UNMEER: 60/092182
PRIOR FILING DATE: 1998-07-07
PRIOR FILING DATE: 1998-07-07
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Best Local
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APPLICANT: Ashker Kevin P.
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Desnoyers, Luc
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Similarity 100.0%; Pred. No. 1.1
Significative 0; Mismatches
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Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Kijavin, Ivar J.
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Gerritsen, Mary E.
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o. 1.9e-08;
o. 0;
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PRICE REILING DANÉ: 1998-06-17
PRICE APPLICATION NUMBER: 60/08959
PRICE REILING DAYE: 1998-06-17
PRICE REILING DAYE: 1998-06-17
PRICE REILING DAYE: 1998-06-18
PRICE REILING DAYE: 1998-06-19
PRICE REILING DAYE: 1998-06-19
PRICE REILING DAYE: 1999-06-19
PRICE REILING DAYE: 1999-06-29
PRICE REILING DAYE: 1999-06
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERRICE: P2730710256

CURRENT APPLICATION NUMBER: US/09/989,279

CURRENT FILING DATE: 2001-11-19

PRIOR PILING DATE: 1997-06-16

PRIOR FILING DATE: 1997-06-16

PRIOR FILING DATE: 1997-01-17

PRIOR APPLICATION NUMBER: 60/06250

PRIOR APPLICATION NUMBER: 60/06250

PRIOR APPLICATION NUMBER: 60/065116

PRIOR APPLICATION NUMBER: 60/065311

PRIOR FILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: 60/066710

PRIOR FILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: 60/066770

PRIOR FILING DATE: 1997-11-24

PRIOR APPLICATION NUMBER: 60/075945

PRIOR APPLICATION NUMBER: 60/075945

PRIOR PILING DATE: 1998-02-25

PRIOR PILING DATE: 1998-02-25

PRIOR PILING DATE: 1998-02-25
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US-09-989-279-407
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PRIOR FILLING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILLING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILLING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILLING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILLING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILLING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILLING DATE: 1998-07-09
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APPLICANT: Baker, Kevin P.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleon
APPLICANT: Fong, Sherman
APPLICANT: Geriber, Hanspeter
APPLICANT: Geriber, Hanspeter
APPLICANT: Geriber, Mary E
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
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Best Local :
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Stewart, Timothy A.
Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
Zhang, Zemin
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Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
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Kljavin, Ivar J
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20020072496A1
NUMBER: 60/078910
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ILING DATE: 1998-06- PELLING DATE: 1998-07-	PPLICATION NUMBER: 60,	FILING DATE: 1998-06-22 APPLICATION NUMBER: 60/02 APPLICATION NUMBER: 60/02 APPLICATION NUMBER: 60/03 APPLICATION NUMBER: 60/03 APPLICATION NUMBER: 60/03 FILING DATE: 1998-06-23 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/0 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/0 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/03	LING DATE: 1998-06-17 LING DATE: 1998-06-17 LING DATE: 1998-06-17 PELCATION NUMBER: 60/ PELCATION NUMBER: 60/ PLICATION NUMBER: 60/ PRICATION NUMBER: 60/

PRIOR FILLING DATE: 1998-03-20
PRIOR FILLING DATE: 1998-04-28
PRIOR FILLING DATE: 1998-05-28
PRIOR FILLING DATE: 1998-05-07
PRIOR PRIDREDATE: 1998-05-07
PRIOR PRIDREDATE: 1998-05-07
PRIOR PELICATION UNMBER: 60/087607
PRIOR PELICATION UNMBER: 60/087607
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PRIOR PELICATION UNMBER: 60/087609
PRIOR PELICATION UNMBER: 60/087609
PRIOR PELICATION UNMBER: 60/080025
PRIOR PELICATION UNMBER: 60/080026
PRIOR PELICATION UNMBER: 60/080027
PRIOR PEL

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APPLICANY: ROY, Margaret Ann
APPLICANY: Stewart, Timothy A.
APPLICANY: Stewart, Timothy A.
APPLICANY: Williams, P. Mickey
APPLICANY: Williams, P. Mickey
APPLICANY: Williams, P. Mickey
APPLICANY: Williams, P. Mickey
APPLICANY: Wood, Williams.
APPLICANY: Wood, William I.
APPLICANY: Wood, William I.
APPLICANY: Zhang, Zemin

TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PLC65
CURRENT APPLICATION NUMBER: US/09/989,727
CURRENT FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/04978
PRIOR APPLICATION NUMBER: 60/062250
PRIOR APPLICATION NUMBER: 60/062250
PRIOR APPLICATION NUMBER: 60/06516
PRIOR APPLICATION NUMBER: 60/06511
PRIOR APPLICATION NUMBER: 60/06511
PRIOR APPLICATION NUMBER: 60/06570
PRIOR PILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/06770
PRIOR PILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR APPLICATION NUMBER: 60/075945
PRIOR APPLICATION NUMBER: 60/078310
PRIOR APPLICATION NUMBER: 60/078312
PRIOR APPLICATION NUMBER: 60/078312
PRIOR APPLICATION NUMBER: 60/078910
PRIOR APPLICATION NUMBER: 60/083322
PRIOR PILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
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US-09-989-727-407
Sequence 407, Application US/09989727
Patent No. US20020072497A1
GENERAL INFORMATION;
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PRIOR APPLICATION NUMBER: 60/09163
PRIOR APPLICATION 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR PRIOR NUMBER: 60/092182
PRIOR APPLICATION NUMBER: 60/092182
PRIOR APPLICATION NUMBER: 60/092182
PRIOR APPLICATION NUMBER: 60/092182
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APPLICANT: Baker, Kevin P.
APPLICANT: Betsein, David
APPLICANT: Botsetein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Earton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
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Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Kljavin, Ivar J.
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PRIOR APPLICATION NUMBER: 60/087607
PRIOR APPLICATION NUMBER: 60/087607
PRIOR APPLICATION NUMBER: 60/087609
PRIOR APPLICATION NUMBER: 60/087609
PRIOR APPLICATION NUMBER: 60/087827
PRIOR APPLICATION NUMBER: 60/088021
PRIOR APPLICATION NUMBER: 60/088021
PRIOR APPLICATION NUMBER: 60/088021
PRIOR APPLICATION NUMBER: 60/088025
PRIOR APPLICATION NUMBER: 60/088026
PRIOR APPLICATION NUMBER: 60/088026
PRIOR APPLICATION NUMBER: 60/088026
PRIOR APPLICATION NUMBER: 60/088026
PRIOR APPLICATION NUMBER: 60/088028
PRIOR APPLICATION NUMBER: 60/088029
PRIOR APPLICATION NUMBER: 60/088030
PRIOR APPLICATION NUMBER: 60/088212
PRIOR APPLICATION NUMBER: 60/0
                                                           PRIOR
                                                                               APPLICATION NUMBER: 60/089538
FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/085598
FILING DATE: 1998-06-17
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FILING DATE: 1998-05-07
APPLICATION NUMBER: 60/
FILING DATE: 1998-05-28
                                    APPLICATION NUMBER: 60/089599 FILING DATE: 1998-06-17
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APPLICANT: Stewart, Time...

APPLICANT: Stewart, Tumes, Daniel

APPLICANT: Watanabe, Colin K.

APPLICANT: Watanabe, Colin K.

APPLICANT: Williams J.

APPLICANT: Williams J.

APPLICANT: Wood, William I.

APPLICANT: Wood, William I.

APPLICANT: Lang, Zemin I.

APPLICANT: Colon, William I.

APPLICANT: Colon, William I.

APPLICANT: Wood, William I.

APPLICANT: 2001-11-20

PRIOR APPLICATION NUMBER: 60/062250

PRIOR APPLICATION WIMBER: 60/065186

PRIOR APPLICATION WIMBER: 60/065311

PRIOR APPLICATION WIMBER: 60/065311

PRIOR APPLICATION WIMBER: 60/06531

PRIOR APPLICATION WIMBER: 60/075945

PRIOR APPLICATION WIMBER: 60/075945

PRIOR APPLICATION WIMBER: 60/078910

PRIOR APPLICATION WIMBER: 60/078910
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US-09-989-731-407
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Matches 78
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Patent No.
GENERAL IN
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PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09
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1 Similarity 100.0%; Pred. No. 1:
78; Conservative 0; Mismatches
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US20020103125A1
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Baker, Kevin P.
Botstein, David
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Eaton, Dan L.
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Gerber, Hanspeter
Gerritsen, Mary E.
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PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089653
PRIOR APPLICATION NUMBER: 60/089801
PRIOR APPLICATION NUMBER: 60/089907
PRIOR APPLICATION NUMBER: 60/089908
PRIOR PRIOR PRICING DATE: 1998-06-19
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OR FILING DATE: 1998-05-28
OR APPLICATION NUMBER: 60/087607
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OR FILING DATE: 1998-06-04
OR APPLICATION NUMBER: 60/088025
OR FILING DATE: 1998-06-04
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OR APPLICATION NUMBER: 60/08823
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OR APPLICATION NUMBER: 60/08823
OR APPLICATION NUMBER: 60/08823
OR APPLICATION NUMBER: 60/08923
OR APPLICATION NUMBER:

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APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Zhang, Zemin
ITILE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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PRIOR APPLICATION NUMBER: 60/062250
PRIOR APPLICATION NUMBER: 60/065186
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/06570
PRIOR APPLICATION NUMBER: 60/075945
PRIOR APPLICATION NUMBER: 60/075945
PRIOR APPLICATION NUMBER: 60/08332
PRIOR APPLICATION NUMBER: 60/08332
PRIOR APPLICATION NUMBER: 60/084600
PRIOR PILING DATE: 1998-03-20
PRIOR PILING DATE: 1998-04-28
PRIOR PILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/08706
PRIOR PILING DATE: 1998-05-07
PRIOR PILING DATE: 1998-06-02
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US-09-989-732-407
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14.2%; Score 78; DB

Best Local Similarity 100.0%; Pred. No. 1.5

Matches 78; Conservative 0; Mismatches
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APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Bestein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerber, Hanspeter
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Nucrey
APPLICANT: Grimaldi, J. Chris:
APPLICANT: Gurney, Austin L.
APPLICANT: Gurney, Austin L.
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PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09
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Gerritsen, Mary E.
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Gurney, Austin L.
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PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/08
PRIOR APPLICATION NUMBER: 60/08
PRIOR FILING DATE: 1998-06-04
PRIOR FILING DATE: 1998-06-04
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                                 PRIOR EPLICATION NUMBER: 60/088029
PRIOR PELING DATE: 1998-06-04
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PRIOR PELING DATE: 1998-06-04
PRIOR PELING DATE: 1998-06-05
PRIOR PELING DATE: 1998-06-10
PRIOR PELING DATE: 1998-06-11
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PRIOR PELICATION NUMBER: 60/089512
PRIOR PELICATION NUMBER: 60/089512
PRIOR PELICATION NUMBER: 60/089512
PRIOR PELICATION NUMBER: 60/089512
PRIOR PELICATION NUMBER: 60/089514
PRIOR PELICATION NUMBER: 60/089512
PRIOR PELICATION NUMBER: 60/089514
PRIOR PELICATION NUMBER: 60/089532
PRIOR PELICATION NUMBER: 60/089532
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PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087759
PRIOR TILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087827
PRIOR APPLICATION NUMBER: 60/088021
PRIOR APPLICATION NUMBER: 60/088021
PRIOR APPLICATION NUMBER: 60/088021
PRIOR FILING DATE: 1998-06-04
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NUMBER: 60: 1998-06-1998-06-18

80/089908

OR APPLICATION NUMBER: 60/089947
OR FILING DATE: 1998-06-19
OR APPLICATION NUMBER: 60/089948
OR FILING DATE: 1998-06-19
OR APPLICATION NUMBER: 60/089952
OR FILING DATE: 1998-06-19
OR APPLICATION NUMBER: 60/090246
OR FILING DATE: 1998-06-22
OR APPLICATION NUMBER: 60/090252
OR APPLICATION NUMBER: 60/090252
OR APPLICATION NUMBER: 60/090254
OR APPLICATION NUMBER: 60/090355
OR APPLICATION NUMBER: 60/09035
OR APPLICATION NUMBER: 60/09035
OR FILING DATE: 1998-06-23
OR APPLICATION NUMBER: 60/09035

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APPLICANT: Baker, Keyin P.
APPLICANT: Botser, Keyin P.
APPLICANT: Botser, Keyin P.
APPLICANT: Botser, Keyin P.
APPLICANT: Botser, Keyin P.
APPLICANT: Beanoyers, Luc
APPLICANT: Beanoyers, Luc
APPLICANT: Codowski, Paul
APPLICANT: Gerber, Hanspeter
APPLICANT: Ray, Americant
APPLICANT: Waliams, P.
APPLICANT: Wood, Waliams, P.
APPLICANT: Waliams, P.
APPLICANT: Wood, Waliams, P.
APPLICANT: Waliam
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US-09-991-073-407
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OR APPLICATION NUMBER: 60/090429
OR FILING DATE: 1998-06-24
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OR APPLICATION NUMBER: 60/090436
OR APPLICATION NUMBER: 60/090444
OR FILING DATE: 1998-06-24
OR APPLICATION NUMBER: 60/090445
OR FILING DATE: 1998-06-24
OR APPLICATION NUMBER: 60/090445
OR FILING DATE: 1998-06-24
OR APPLICATION NUMBER: 60/090540
OR APPLICATION NUMBER: 60/090540
OR FILING DATE: 1998-06-24
OR APPLICATION NUMBER: 60/090540
OR APPLICATION NUMBER: 60/09057
OR FILING DATE: 1998-06-24
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OR APPLICATION NUMBER: 60/09067
OR FILING DATE: 1998-06-25
OR APPLICATION NUMBER: 60/09067
OR FILING DATE: 1998-06-25
OR APPLICATION NUMBER: 60/09069
OR FILING DATE: 1998-06-25
OR APPLICATION NUMBER: 60/09069
OR APPLICATION NUMBER: 60/090863
OR APPLICATION NUMBER: 60/090863
OR APPLICATION NUMBER: 60/09154
OR APPLICATION NUMBER: 60/09159
OR APPLICATION NUMBER: 60/09159
OR APPLICATION NUMBER: 60/09159
OR APPLICATION NUMBER: 60/09162
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Matches

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Query Match 14.2%; Score 78; DB Best Local Similarity 100.0%; Pred. No. 1.9 Matches 78; Conservative 0; Mismatches

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Length 570;;
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Gaps

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APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C25
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Godowski, Paul J.
Grimaldi, J.Christopher
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Gerritsen, Mary E
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| PRIOR PELLING DATE: 1998-06-25
| PRIOR PELLING DATE: 1998-07-20
| PRIOR PELLING DATE: 199
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Search completed: September 20, 2003, 03:21:37 Job time:  $220.634 \ \text{secs}$ 

Run on: OM nucleic -

Title: Perfect score:

Scoring table: Sequence:

Database

Result No.

Score

308.8 308.8 308.8 308.8 308.8 308.8 308.8

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Post-processing: Minimum Match 0%
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Maximum DB seq length: 2000000000
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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2: /SIDS1/gcgdata/gen
3: /SIDS1/gcgdata/gen
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| SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
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AAZ98173
AAZ29723
AAV54620
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      AAZ65103
AAF44249
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Novel human secret
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30-OCT-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LU105; lung disease marker; immunoassay; lung disease; cancer;
blood; plasma; serum; ss
                                                                                     31-JAN-1997;
                                                                                                                                                                                             06-AUG-1998.
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79..393
/*tag= a
/transl_except= (pos:136..138, aa:Val)
/product= "LU105 polypeptide"
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ABX81273
ABX99363
ABX77974
ABX754618
ABX17173
ABX54618
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AAV38067
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AAV38067
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ABX16707

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Lung cancer relate pol-
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RESULT 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 310
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Granados EN,
Russell JC, S
    11-MAY-2000
                                                                                        AAZ98173 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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les 310; Conservat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 519 BP; 78 A; 190 C; 170 G; 81 T; 0 other;
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lpe SD;
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                                                                                          543
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                                                                                          ВP
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Pred. No. 4.5e-53;
0; Mismatches 2
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Query Match Best Local S Matches 310

310; Conserv

Conservative

99.0%;

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; ;.5e-53; 2;

Indels Length

0;

Gaps

0;

Sequence

543

BP;

89 A; 194 C;

178 G; 82 T;

0 other; DВ 21;

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CC human signal peptide-containing proteins HSPP-1 to HSPP-134. HSPPs have canticancer, anti-inflammatory, antimicrobial, nootropic, hepatotropic, canticancer, anti-inflammatory, antimicrobial, nootropic, hepatotropic, cassociated with decreased activity or function of HSPP. Antagonists of CC activity or function of HSPP. Such diseases include cell proliferation cativity or function of HSPP. Such diseases include cell proliferation comproductive or developmental disorders associated with increased cc irrhosis, psoriasis, acquired immune deficiency syndrome, anaemia, CC reproductive or developmental disorders, (e.g. arteriosclerosis, cc irrhosis, psoriasis, acquired immune deficiency syndrome, anaemia, CC asthma, Crohn's disease, microbial or other infections, congestive or clischaemic heart disease, Alzheimer's, parkinson's or Huntington's CC diseases, Schizophrenia, ovulatory defects, muscular dystrophy). HSPP CC nucleic acids can be used for the recombianant production of HSPP, for Cd detecting HSPP in standard hybridisation and amplification assays (for CC tiphex-forming or ribozyme therapeutics, for detecting related sequences CC or genetic variations, and for chromosomal mapping. HSPP are also used to craise specific antibodies (Ab) and to screen for agonists and antiponists, in competitive drug screens, and for purification of HSPP cromostrus, in competitive drug screens, and for purification of HSPP cromostrus, in competitive drug screens, and for purification of HSPP cromostrus, in competitive drug screens, and for purification of HSPP cromostrus, in competitive drug screens, and for purification of HSPP cromostrus.
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31-JUL-1998;
01-OCT-1998;
11-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New human signal peptide-containing proteins useful in treatment, prevention and diagnosis of e.g. cancer, inflammation and cardiovascular disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lal P, 1
Akerblom
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; signal peptide-containing protein; HSPP; diagnosis; cancer; inflammation; cardiovascular disease; anticancer; anti-inflammatory; antimicrobial; nootropic; neuroprotective; cardiovascular; hepatotropic; antiasthmatic; gene therapy; cell proliferation; neurological disorder; reproductive disorder; developmental disorder; arteriosclerosis; cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia; asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia; asthma; Crohn's disease; Huntington's disease; ovulatory defect; machine disease; disease; Huntington's disease; ovulatory defect;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human signal peptide containing protein HSPP-65
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om IE,
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                                         sources.
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98US-0094983.
98US-0102686.
98US-0112129.
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Young J, Yue
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R, Hillman
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Query Match
                                  The present sequence is a lung specific gene (LSG) Lng107 from human clone ID 586271. The LSG has high level of tissue specificity for lungs and is overexpressed in cancerous tissues. The sequence serves as a diagnostic marker for detecting, monitoring, staging and prognosticating lung cancer. The diagnostis involves comparing levels of LSG in samples obtained from patient and normal control.
                                                                                                                                                                                                                                                                                                                                                                                                                                          AAZ29723 standard; DNA; 543
                                                                                                                                                                     Yang F,
                                                                                                                                                                                                                                                                  WO9960160-A1
                                                                                                                                                                                                                                                                                                                                                                                 Human lung specific gene Lng107.
                                                                                                                                                                                                                                                                                                                                                                                                     27-MAR-2000
                  Sequence
                                                                                                     Claim 6; Page 36; 40pp; English.
                                                                                                                      A new method for diagnosing, monitoring and staging lung cancer
                                                                                                                                            P-PSDB;
                                                                                                                                                                                                            21-MAY-1998;
                                                                                                                                                                                                                             12-MAY-1999;
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                                                                                                                                           AAY44458.
                                                                                                                                                                                         DIADEXUS LLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTGAGCAGCCTGGGCATCCCCGTGAACCACCTCATAGAGGGCTCCCAGAAGTGTGTGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAGGCCGGGGCCGGGACCCTGGCCAACCCCTCGGCACCCTCAACCCGCTGAAGCTCCTGGAGGCCTGGAAGCTCCTGGCAACCCGCTGAACCCGCTGAAGCTCCTGGAAGCTCCTGGAAGCTCCTGAACCCGCTGAAGCTCCTGAAGCTCCTGAAGCTCCTGAAGCTCCTGAAGCTCCTGAAGCTCCTGAAGCTCCTGAAGCTCTGAAGCTCTGAAGCTC
                  543 BP;
                                                                                                                                                                     Macina RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACAGTGTTTGGC 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACAGTGTTTGGC 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAGCTGGGTCCCCAGGCCGTGGGGGCCCGTGAAGGCCCCTGAAGGCCCTGCTGGGGGCCCCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                     Gene;
;; lung
                                                                                                                                                                                                           980S-0086212
                                                                                                                                                                                                                             99WO-US10344.
                                                                                                                                                                                                                                                                                   /product=
                                                                                                                                                                                                                                                                                                        Location/Qualifiers 93..407
                 89 A; 194 C; 178 G; 82 T;
                                                                                                                                                                                                                                                                                               /*tag=
                                                                                                                                                                                                                                                                                                                                                      LSG; Lng
cancer;
                                                                                                                                                                       Sun
 99.0%;
                                                                                                                                                                                                                                                                                                                                                      Lng107; human
er; diagnosis;
                                                                                                                                                                       ۲
                                                                                                                                                                                                                                                                                     "LSG Lng107
                                                                                                                                                                                                                                                                                                                                                                                                                                           ВP
Score 308.8;
                                                                                                                                                                                                                                                                                                                                                                human;
                                                                                                                                                                                                                                                                                    protein"
                                                                                                                                                                                                                                                                                                                                                       ds.
DB
                  0 other;
21;
Length 543;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120
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RESULT 4

ANYS46200
ID AAVS

XX AAVS

XX LU11

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Qγ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Qy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 99.48; Matches 310; Conservative
                                                                                                                                                 WPI; 199
P-PSDB;
                                                                                                                                                                                                                 Billing-medel PA, Cohen Granados EN, Hodges SC, Russell JC, Stroupe SD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LU105;
blood;
                    Claim 11; Fig
                                                      New nucleic acid for the lung disease marker LU105 - polypeptides, antibodies and genes, used for diagnosis, prevention, treatment of lung disease, specifically cancer
                                                                                                                                                                                                                                                                                                          (ABBO ) ABBOTT
                                                                                                                                                                                                                                                                                                                                                      31-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                  30-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                           06-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9833926-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LU105 specific consensus polynucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-MAR-2003
30-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAV54620;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAV54620 standard; cDNA; 562
                                                                                                                                                      1998-437479/37.
DB; AAW75868.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 GAGGCCGGGGCCGGGACCCTGGCCAACCCCTCGGCACCCTCAACCCGCTGAAGCTCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        153 TICTTAGTGGGCTCGGCCAAGCCTGTGGCCCAGCCTGTGCGTGGGGTGGAGTCGGCGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     393
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ATGAAGCTCGCCGCCCTCCTGGGGCTCTGCGTGGCCCTGTCCTGCAGCTCCGCTGCTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lung disease marker;
plasma; serum; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACAGTGTTTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GACCTGGGTCCCCAGCCCTGGGGGCCCGTAAAGGCCCTGAAGGCCCTGCTGGGGGCCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTGAGCAGCCTGGGCATCCCCGTGAACCACCTCATAGAGGGCTCCCCAGAACTGTGTGGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAGGCCGGGGCCGGGACCCTGGCCAACCCCCTCGGCACCCTCAACCCCGCTGAAGCTCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTCTTAGTGGGCTCGGCCAAGCCTGTGGCCCAGCCTGTCGCTGCGCTGGAGTCGGCGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (updated)
(first entry)
                    1; 123pp; English
                                                                                                                                                                                                                                                                                                          LAB.
                                                                                                                                                                                                                                                                                                                                                      97US-0791710
                                                                                                                                                                                                                                                                                                                                                                                                  98WO-US01766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /transl_except= (pos:176..178, aa:Val) .
/product= "LU105 polypeptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     404
                                                                                                                                                                                                                                         M, Colpitts
Klass MR, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immunoassay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 4.5e-53;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP
                                                                                                                                                                                                                                         s TL, Friedman PN, Gordon J;
Kratochvil JD, Robertsrapp L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lung disease; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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Qy
dd
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cc Sequences shown in AAV$4616 to AAV$4621 represent LU105 specific polynucleotide sequences. These are used in the method of the invention composition and the sequences of the invention composition and the sequences of the composition and the sequences that least one LU105 specific nucleic acid, or its complement complete with at least one LU105 specific nucleic acid, or its complement complete with its at least 50 percent identical with the LU105 specific nucleic acid sequences (AAV$4616 to AAV$4621). LU105 is a lung disease marker call transformed with a recombinant expression system that contains complete complete with a recombinant expression system that contains cullofs specific nucleic acid fragments, are used to express recombinant cullofs specific antibodies, in usual immunoassays. The antibodies are used to detect the LU105 antigen, and correspondingly this antigen is cused to detect specific antibodies, in usual immunoassays. The LU105 constitution, prognosis, prevention, treatment and determination of susceptibility to, lung disease, specifically cancer. The LU105 concentration, in altered form or in an unusual body compartment). LU105 can be detected in blood, plasma or serum in an inexpensive, non-invasive can be detected in blood, plasma or serum in an inexpensive, non-invasive.
                                                                                                                                                                                                                                                                                                                                                              В
                                                                                                                                                                                                                                                                                                                                                                                QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                         Human; PRO; benign tumour; malignant tumour; lymphoid malignancy; leukaemia; neuronal disorder; stromal disorder; blastocoelic disorder; inflammatory disorder; immune disorder; anglogenic disorder; gene therapy; cytostatic; neuroprotective; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Updated on 25-MAR-2003 to correct PI field.)
                                                                                                                                                                                       cDNA encoding human
                                                                                                                                                                                                                      15-JUL-2002
                                                                                                                                                                                                                                                                                   ABK40267 standard;
                                                                               Homo sapiens
                                                WO200153486-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       310;
                                                                                                                                                                                                                                                                                                                                                                                       301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATGAAGCTCGCCÓCCCTCCTGGGGCTCTGCGTGGCCCTGTCCTGCAGCTCCGCTGCT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 562
                                                                                                                                                                                                                                                                                                                                                                                                                        GAGCTGGGTCCCCAGGCCGTGGGGGCCCTGAAGGCCCTGAAGGCCCTGCTGGGGGCCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTCTTAGTGGGCTCGGCCAAGCCTGTGGCCCAGCCTGTCGCTGCGCTGGAGTCGGCGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTGAGCAGCCTGGGCATCCCCGTGAACCACCTCATAGAGGGCTCCCAGAAGTGTGTGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAGGCCGGGGCCGGGACCCTGGCCAACCCCTCGGCACCCTCAACCCCGCTGAAGCTCCTG
                                                                                                                                                                                                                                                                                                                                                            ACAGTGTTTGGC 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTGAGCAGCCTGGGCATCCCGTGAACCACCTCATAGAGGGCTCCCAGAAGTGTGTGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAGGCCGGGGCCGGCCAACCCCCTCGGCACCCTCAACCCGCTGAAGCTCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTCTTAGTGGGCTCGGCCAAGCCTGTGGCCCAGCCTGTCGCTGGAGTCGGCGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99.0%;
llarity 99.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP; 82 A;
                                                                                                                                                                                                                      (first
                                                                                                                                                                                                                                                                                   CDNA;
                                                                                                                                                                                     PRO1245 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 200 C; 192 G; 86 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 308.8; DB 19;
Pred. No. 4.5e-53;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                     ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 562;
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QΥ
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                     Qy
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Best Local S
Matches 310
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22-JUN-1999
20-JUL-1999
26-JUL-1999
28-JUL-1999
17-AUG-1999
31-AUG-1999
31-SEP-1999
31-SEP-1999
30-NOV-1999
01-DEC-1999
01-DEC-1999
01-DEC-1999
01-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-MAR-1999;
11-MAR-1999;
11-MAY-1999;
02-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ashkenazi AJ,
Marsters SA,
Watanabe CK,
                                                                                                                                                                                                                                                                                                                       The present invention relates to the isolation of novel human PRO polypeptides and the polynucleotide sequences encoding them. The PRO polypeptides, agonists, antagonists or anti-PRO antibodies are useful for treating benign or malignant tumours (e.g. renal, kidney, bladder, breast, etc), leukaemias and lymphoid malignancies, other disorders such as neuronal, glial, astrocytal, hypothalamic, glandular, macrophagal, stromal and blastocoelic disorders, inflammatory, immune and angiogenic disorders. The polynucleotide sequences are also useful in gene therapy. ABK40254-ABK40288 encode for the human PRO polypeptides of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thirty five nucleic acids encoding PRO polypeptides, useful for treating benign or malignant tumours, leukaemias and lymphoid malignancies, inflammatory, angiogenic and immunologic disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 50; Fig 27; 302pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2002-205567/26.
DB; AAU86141.
                                                                          181
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                                                                                                                           121
                                                                                                                                                    139
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310; Conservative
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                                                CTGAGCAGCCTGGGCATCCCCGTGAACCACCTCATAGAGGGCTCCCAGAAGTGTGTGGCT
                                                                                                                GAGGCCGGGGCCGGGACCCTGGCCAACCCCCTCGGCACCCTCAACCCGCTGAAGCTCCTG
                                                                                                                                                 TTCTTAGTGGGCTCGGCCAAGCCTGTGGCCCAGCCTGTCGCTGCGCTGGAGTCGGCGGCG
                                                                                                                                                                TTCTTAGTGGGCTCGGCCAAGCCTGTGGCCCAGCCTGTCGCCTGCGCTGGAGTCGGCGCG
                                                                                                                                                                                                 569 BP; 128 A; 190 C; 170 G; 81 T; 0 other;
                GAGCTGGGTCCCCAGGCCGTGGGGGGCCGTGAAGGCCCTGAAGGCCCTGCTGGGGGGCCCTG
GAGCTGGGTCCCCAGGCCGTGGGGGCCCTGAAAGGCCCTGCTGGGGGCCCCTG
                                                                                                 GAGGCCGGGGGCCCTGGCCAACCCCTCGGCACCCTCAACCCGCTGAAGCTCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99WO-US12252

99US-140650P

99US-140650P

99US-140650P

99US-140650P

99US-140650P

99US-14508P

99US-14508P

99US-151609P

99US-151609P

99WO-US21011

99WO-US21011

99WO-US21011

99WO-US28301

99WO-US28301

99WO-US28301
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Pan J, Pitti RM,
Wood WI;
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99US-123972P
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[ RM, Roy MA,
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                                                                                                                                                                                                                                                   Score 308.8; DB Pred. No. 4.5e-53 O; Mismatches
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Smith
                                                                                                                                                                                                                                                                             24; Length
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Stone DM;
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                                                                                                                                                                                                                                                      Gaps
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PR 19-JUN-1998 PR 22-JUN-1998 PR 22-JUN-1998 PR 23-JUN-1998 PR 23-JUN-1998 PR 24-JUN-1998 PR 25-JUN-1998 PR 25-	17 - JUN - 1998; 17 - JUN 1998; 17 - JUN 1998; 17 - JUN 1998; 17 - JUN 1998; 18 - JUN 1998; 18 - JUN 1998; 18 - JUN 1998; 19 - JUN 1998;	10-JUN-1998; 10-JUN-1998; 11-JUN-1998; 11-JUN-1998; 11-JUN-1998; 11-JUN-1998; 11-JUN-1998; 12-JUN-1998; 12-JUN-1998; 16-JUN-1998; 16-JUN-1998; 16-JUN-1998;	PR 05-JUN-1998; 98US-0088167, PR 05-JUN-1998; 98US-0088202. PR 05-JUN-1998; 98US-0088202. PR 05-JUN-1998; 98US-0088217. PR 05-JUN-1998; 98US-0088217. PR 09-JUN-1998; 98US-0088217. PR 10-JUN-1998; 98US-0088730. PR 10-JUN-1998; 98US-0088730. PR 10-JUN-1998; 98US-0088738. PR 10-JUN-1998; 98US-0088738. PR 10-JUN-1998; 98US-0088741.	02-JUN-1998 02-JUN-1998 02-JUN-1998 03-JUN-1998 03-JUN-1998 04-JUN-1998 04-JUN-1998 04-JUN-1998 04-JUN-1998 04-JUN-1998 04-JUN-1998	KW pharmaceutical; receptor immunoadhesin; gene mapping; ss.  XX OS Homo sapiens.  XX PN W09963088-A2.  XX PD 09-DEC-1999.  XX PF 02-JUN-1999; 99WO-US12252.	379 ACAGTGTTTGGC 390  SULT 6 Z65103 AAZ65103 standard; cDNA; 570 BP.  AAZ65103;  05-APR-2000 (first entry)  Membrane-bound protein PRO1245 encoding cDNA.
	17 - AUG- 17 - AUG- 17 - AUG- 17 - AUG- 17 - AUG- 18 - AUG- 18 - AUG- 18 - AUG- 18 - AUG- 19 - AUG-	04 - AUG- 10 - AUG- 10 - AUG- 10 - AUG- 11 - AUG- 11 - AUG- 11 - AUG- 11 - AUG- 17 - AUG- 17 - AUG- 17 - AUG-	02-JUL- 02-JUL- 02-JUL- 07-JUL- 07-JUL- 09-JUL- 109-JUL- 20-JUL- 20-JUL- 20-JUL- 30-JUL- 30-AUG- 04-AUG- 04-AUG- 04-AUG- 04-AUG- 04-AUG- 04-AUG- 04-AUG- 04-AUG- 04-AUG- 04-AUG- 04-AUG- 04-AUG- 04-AUG- 04-AUG- 04-AUG- 04-AUG- 04-AUG- 04-AUG- 04-AUG- 04-AUG- 04-AUG- 04-AUG- 04-AUG- 04-AUG- 04-AUG-	25 JUN 26 JUN 26 JUN 21 JUN 01 JUL 01 JUL 02 JUL 02 JUL 02 JUL 02 JUL 02 JUL 02 JUL 02 JUL	24 - JUN - 24 - JUN - 25 - JUN -	19-JUN- 22-JUN- 22-JUN- 23-JUN- 23-JUN- 24-JUN- 24-JUN- 24-JUN- 24-JUN- 24-JUN- 24-JUN- 24-JUN- 24-JUN- 24-JUN-

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Best Local S
Matches 310
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24-AUG-1998
26-AUG-1998
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31-AUG-1998
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31-AUG-1998
                                                                                                                                                                                                                                                                                                                  The invention provides membrane-bound PRO polypeptides and polynucleotides encoding them. The PRO sequences of the invention were identified based on extracellular domain homology screening. The PRO sequences have homology with proteins including IDL receptors, TIE ligands and various enzymes. The membrane-bound proteins and receptor molecules are useful as pharmaceutical and diagnostic agents. Receptor immunoadhesins, for instance, can be used as therapeutic agents to block receptor-ligand interactions. The membrane-bound proteins can also be employed for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. The PRO encoding sequences are useful as hybridization probes, in chromosome and gene mapping and in the generation of antisense RNA and DNA. PRO nucleic acid sequences will also be useful for the preparation of PRO polypeptides, especially by recombinant techniques.
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P-PSDB;
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Wood V
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                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                             recombinant techniques.
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ACAGTGTTTGGC
            ACAGTGTTTGGC
                                        GAGCTGGGTCCCCAGGCCGTGGGGGCCCTGAAGGCCCTGAAGGCCCTGCTGGGGGCCCTG
                                                   GAGCTGGGTCCCCAGGCCGTGGGGGCCCTGAAGGCCCTGCTGCTGCGGGGCCCTG
                                                                                CTGAGCAGCCTGGGCATCCCCGTGAACCACCTCATAGAGGGCTCCCAGAAGTGTGTGGCT
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Yuan
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98US-009761.
98US-0097951.
98US-0097952.
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98US-0097971.
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98US-0097980.14.
98US-00979865.
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                    312
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                                                                                                                                                                                                                                                                                        G;
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.5e-53;
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23-JUN-1999
23-JUN-1999
20-JUL-1999
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26-JUL-1999
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17-AGG-1999
17-AGG-1999
17-AGG-1999
18-SEP-1999
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16-DEC-1999
30-NOV-1999
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30-NOV-1999
16-DEC-1999
16-DEC
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99US-0144758
99US-0145698
99US-0145996
99US-0149396
99WO-US21190
99WO-US211547
99US-0158653
99WO-US20159
99WO-US2015
99WO-US2015
2000WO-US00219
2000WO-US00219
2000WO-US00216
2000WO-US04341
2000WO-US04414
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2000WO-US05804
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99US-0141037
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Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Grimaldi CJ, Gurney AL, Kljavin IJ, Napier MA, Pan J, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Godowski | Paoni NF; Wood WI; рJ;

WPI; 2001-032160/04. P-PSDB; AAB65280.

PRO polynucleotides used bioactive molecules such specific cells, to cause to produce polypeptides as toxins, radiolabels c targeted cell death or antibodies, ť

Claim 2; Fig 289; 935pp; English.

The present invention describes human secreted and transmembrane PRO proteins. The PRO proteins have cytostatic activity. The PRO proteins can be used for targeted delivery of bioactive molecules, such as toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide sequences, and their fragments, can be used as hybridisation probes, in chromosomal and gene mapping, and in the generation of anti-sense RNA and DNA. They may also be used to produce transgenic animals which are used to develop and screen therapeutically useful reagents. The PRO

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  05-NOV-1997;
16-SEP-1998;
17-SEP-1998;
07-OCT-1998;
01-DEC-1998;
05-JAN-1999;
                                                                                                                                                                                                                                                                                                                    Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing; cardiac insufficiency disorder; cancer; tumour; immune response; adrenal cortical capillary endothelial growth; c-fos induction; vascular endothelial growth factor inhibition; VEGF inhibition; endothelial cell growth inhibitor; T-lymphocytes stimulation; retinal neurons cell survival; rod photoreceptor cell survival; rad photoreceptor cell survival; mammalian kidney mesangial cell proliferation; Berger disease; denondrocyte proliferation; chondrocyte redifferentiation; sports injury; arthritis; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleotide and protein sequence can be used for tissue typing and in treating cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to AAF44470 represent PCR primers and hybridisation probes us in the isolation of human PRO sequences. AAF44087 to AAF44269 and AAB65154 to AAB65300 represent human PRO polynucleotide and protein sequences given in the exemplification of the present invention.
                                                                                                                                                 14 - NOV - 2001;
                                                                                                                                                                                                19-SEP-2002
                                                                                                                                                                                                                                         US2002132252-A1
                                                                                                                                                                                                                                                                                   Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel human secreted or transmembrane protein PRO1358 DNA.
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al Similarity 99.4%;
310; Conservative
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                                                                                                                                                      2001US-0990442
  97WO-US20069.
98WO-US19437.
98WO-US19437.
98WO-US21141.
98WO-US25108.
99WO-US00106.
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17-DEC-1998
10-JUN-1998
11-JUN-1998
99WO-USCO20

12000WO-USCO20

12000WO-USCO20
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378 300 318 240 258 180 198

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Crimbellial growth factor (VEGF) stimulate proliferation of cells and setular and are thus and setular dependence of stimulate string endothelial cells, pro0186 and setulate and are thus cells and setulate are considered and therefore are useful for treating conditions or disorders where angiopeptide are thus cells and setulate are considered and the thus cells and is thus cells and pro1387 induce c-fos in endothelial growth, and pro336, cell pro1386 and pro1387 induce c-fos in endothelial growth, and pro1387 pro1386 are pro1386 or pro535, pro8150 and pro1387 induce c-fos in endothelial growth, and pro536, cells setul for treating conditions or disorders where angiopenesis would be beneficial, e.g. wound healing and antagonist of this polypeptide are cells and is thus useful for inhibiting endothelial cells, and are thus cells and is thus useful for inhibiting endothelial cell growth in cells and is thus useful for inhibiting endothelial cell growth. Pro826, pro1068, pro1184, pro1346 and pro1375 stimulated proliferation of endothelial cell growth in cells in inhibiting tumour growth. Pro826, cells and in the profile are profileration of cells in inhibiting endothelial cell growth in pro826, cells inhibiting endothelial cell growth in pro1368 or pro1368, pro1328, pro132
                                                                                                                                          Query Match
Best Local Similarity
Matches 310; Conserv
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16-JUN-1998
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Ferrara N,
Grimaldi J
Roy MA, S
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P-PSDB;
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N, Fong S, Gerber H, Gerritsen ME, Goddard A,
JC, Gurney AL, Kljavin LJ, Napier MA, Pan J,
Stewart TA, Tumas D, Watanabe CK, Williams PM,
                                                                                                                                                                                                                                                                   570
                 98US-089105P

98US-08944P

98US-089514P

98US-089538P

98US-089538P

98US-089598P

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98US-089908P
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ilarity 99.4%;
Conservative
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98WO-US19437
98WO-US21141
98WO-US25108
99WO-US25108
99WO-US2028
99WO-US2028
99WO-US28313
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2000WO-US063681
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Best Local Similarity 99.4%;
Matches 310; Conservative
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22-DEC-1998;
12-MAR-1999;
23-JUN-1999;
05-NOV-1997
16-SEP-1998
17-SEP-1998
07-OCT-1998
01-DEC-1998
05-JAN-1999
05-JAN-1999
02-JUN-1999
15-SEP-1999
15-SEP-1999
                                                                                                                                                                                                                                                                                   Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing cardiac insufficiency disorder; cancer; tumour; immune response; adrenal cortical capillary endothelial growth; c-fos induction; vascular endothelial growth factor inhibition; VEGF inhibition; endothelial cell growth inhibitor; T-lymphocytes stimulation; retinal neurons cell survival; rod photoreceptor cell survival; rod photoreceptor cell survival; rad photoreceptor cell survival; retinal disorder; retinitis pigmentosum, kidney disorder; mammalian kidney mesangial cell proliferation; Berger disease; denondrocyte proliferantial; Crohn's disease; chondrocyte proliferantial; sports injury; arthritis; gene; ds.
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98US-113296P.
99US-123957P.
99US-141037P.
   97WO-US20069.
98WO-US1930.
98WO-US19437.
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        99WO-US28313

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99WO-US300376

2000WO-US30541

2000WO-US05841

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2000WO-US06843

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2000WO-US23782

2000WO-US23322

2000WO-US2
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RESULT 11
ABX90363
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XX ABX90
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Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Zhang Z; 1 DL; Godowski PJ; Paoni NF; 1, Wood WI;

WPI; 2003-288106/28. P-PSDB; ABU60604.

New transmembrane polypeptides and nucleic acids encoding the polypeptides, useful in gene therapy, in chromosome identification, chromosome markers, or in generating probes as

Claim Fig 289; 650pp; English.

The invention discloses isolated PRO secreted/transmembrane polypeptides CC comprising a sequence without signal peptide and the nucleic acid cencoding them. The polypeptides can be used to raise antibodies that CC encoding them. The polypeptides can be used to raise antibodies that CC specifically bind to the PRO polypeptide, for linking a bloactive CC molecule to a cell expressing a PRO protein and for modulating at least CC one biological activity of a cell. The PRO polypeptides or polynucleotides are also useful in gene therapy, in chromosome CC identification, as chromosome markers, or in generating probes. The PRO polypeptides are useful as molecular markers for protein CC electrophoresis, and the isolated nucleic acids may be used for cecombinantly expressing those markers. The PRO polypeptides are useful in diagnostic assays for PRO, and in affinity purification of PRO from CC acids may also be used in tissue typing. Anti-PRO antibodies are useful in diagnostic assays for PRO, and in affinity purification of PRO from CC acids may also be used in tissue typing. Anti-PRO antibodies are useful in diagnostic assays for PRO, and in affinity purification of PRO from CC acids may also are the genes encoding, the primers amplifying and the CC probes detecting the PRO polypucleotides of the invention.

CC PROSE THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE DATA SECUENCE. The sequence at a sequence of the invention.

BP; 129 A; 190 C; 170 G; 81 T; 0 other;

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301 AC 12 379 AC 11 379 AC 11 379 AC 11 12 44-APR-2003 11 12 144-APR-2003 147-2003 147-2003 15-NOV-2001 15-EB-2003 15-NOV-2001 16-EB-2003 16-EC-1998 16-DC-1998 16-DC-1998 16-DC-1998 16-DC-1998 16-DC-1998 16-DC-1998 16-DC-1999 16-DC	241 GAG     319 GAG
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Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A,
Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J,
Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CC omprising a sequence without signal peptide and the nucleic acid ce encoding them. The polypeptides can be used to raise antibodies that CC specifically bind to the PRO polypeptide, for linking a bioactive conclude to a cell expressing a PRO protein and for modulating at least CC one biological activity of a cell. The PRO polypeptides or polynucleotides are also useful as pharmaceuticals, diagnostics, CC polynucleotides are also useful as pharmaceuticals, diagnostics, CC polynucleotides are also useful as pharmaceuticals, diagnostics or bioseancors or bioreactors, for detecting or treating e.g. tumours in CC mammals, e.g. humans, dogs, cats, cattle, horses, sheep, pigs, goats or CC rabbits as targets for therapeutic intervention in certain cancers (e.g. CC colon, lung or breast cancers) and diagnostic determination of the CC presence of these cancers. The PRO polypeptides are also useful as molecular weight markers or for chromosome identification. The PRO genes CC CDNA, genomic DNA or mRNA. The PRO genes may also be used in gene CC therapy, particularly for replacing a defective gene. The sequences CC amplifying and the probes detecting the PRO polynucleotides of the CC invention.

CC Note: The sequence data for this patent is also available in electronic CC format from USPTO at sequence. html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 310
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P-PSDB;
                          cDNA encoding human PRO1245 polypeptide
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                                                                            26-FEB-2003
                                                                                                                           ABX64209;
                                                                                                                                                                          ABX64209 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 570 BP; 129 A; 190 C; 170 G; 81 T; 0 other;
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DB; ABU59026.
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illarity 99.4%;
Conservative
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                                                                         entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 308.8; DB 25;
Pred. No. 4.5e-53;
0; Mismatches 2;
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0, Gaps

378

318 240 258 180 198 120 138

Human; PRO pol genetic disord gene therapy;

US2002103125-A1

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PRO polypeptide; secreted c disorder; antibacterial;
97WO-US20069
98WO-US219330
98WO-US19337
98WO-US19337
98WO-US19330
98WO-US21141
98WO-US21166
99WO-US251090
99WO-US251090
99WO-US251090
99WO-US251090
99WO-US251090
99WO-US268313
299WO-US30591
2000WO-US30591
2000WO-US04141
2000WO-US04141
2000WO-US04141
2000WO-US05411
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2000WO-US05414
2000WO-US13358
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immunosuppressive; transgenic;
        The present invention relates to the isolation of novel human PRO CC polypeptides, and the polynucleotide sequences encoding them. The CC propertides are useful for detecting other propertides. The PRO CC linking bioactive molecules to cells expressing PRO polypeptides, for CC linking bioactive molecules to cells expressing PRO polypeptides, for CC polypeptides, and for for identifying agonists or antagonists. The propertides are useful as CC polypeptides, and for for identifying agonists or antagonists. The propertides are useful as CC polypeptides, and for the propertides are useful as CC polypeptides, and for the propertide and gene mapping, in the generation CC of antisense RNA and DNA, in the preparation of PRO polypeptides, for CC polypeptide, and for the genetic analysis of individuals with genetic CC polypeptide, and for mapping the gene which encodes the PRO CC golypeptide, and for the genetic analysis of individuals with genetic CC disorders, in gene therapy, for chromosome identification, as CC chromosome markers, and for generating probes for PCR, Northern CC sequence encodes a human PRO polypeptide of the invention. CC sequence encodes a human PRO polypeptide of the invention. CC format directly from the USPTO web site at CC sequence data for this patent was obtained in electronic CC sequence data for this patent was obtained in electronic CC sequence and properties and properties at the sequence data for this patent was obtained in electronic CC sequence data for this patent was obtained in electronic CC sequence data for this patent was obtained in electronic CC sequence data for this patent was obtained in electronic CC sequence data for this patent was obtained in electronic CC sequence data for this patent was obtained in electronic CC sequence data for this patent was obtained in electronic CC sequence data for this patent was obtained in electronic CC sequence data for this patent was obtained in electronic CC sequence data for this patent was obtained in electronic CC content of the content
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Ferrara N, Fong S, G
Grimaldi JC, Gurney A
ROY MA, Stewart TA,
        Sequence
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11-JUN-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim
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P-PSDB; ABU13986.
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        BP;
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98US-088030P.
98US-088033P.
98US-088033P.
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98US-088212P.
98US-088212P.
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98US-089514P.
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98US-08953P.
98US-08950P.
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     190
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other;
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Godowski | Paoni NF; Wood WI;

рJ;

15-SEP-1998
17-SEP-1998
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07-0CT-1998; 01-DEC-1998; 05-JAN-1999; 08-MAR-1999; 02-JUN 1999; 15-SEP-1999; 15-SEP-1999; 16-DEC-1999; 01-DEC-1999; 16-DEC-1999; 16-DEC-1999; 16-DEC-1999; 16-JAN-2000; 20-DEC-1999; 16-JAN-2000; 21-FEB-2000; 22-FEB-2000; 23-FEB-2000; 23-FE	Human PRO polynux toxin; radiolabel protein electropi antibacterial. Homo sapiens. US2002123463-A1. 05-SEP-2002. 19-NOV-2001; 200: 05-NOV-1997; 9: 16-SEP-1998; 9: 17-SEP-1998; 9:	RESULT 15 ABX17173 ID ABX17173 standard; XX AC ABX17173; XX DT 04-FEB-2003 (firs	181 CTGAGC	Query Match Best Local Similari Matches 310; Cons.  1 ATGAAGC                     b
98WO-US21141. 98WO-US25108. 99WO-US05028. 99WO-US2522. 99WO-US21547. 99WO-US21547. 99WO-US21547. 99WO-US21541. 99WO-US21541. 99WO-US21541. 99WO-US2155. 99WO-US21565. 2000WO-US01565. 2000WO-US01565. 2000WO-US01565. 2000WO-US01565.	RO polynucleotide #127.  PRO; gene; ss; secreted polypeptide; transmembrane polypeptide; radiolabel; cell death; gene mapping; chromosome mapping; electrophoresis; genetic disorder; immunosuppressive; cytostatic; terial.  plens. plens. plens. 23463-A1. 2002. 2001; 2001US-0989732. 1998; 98WO-US20069. 1999; 97WO-US20069. 1998; 98WO-US19330.	ard; cDNA; 570 BP.	CTGAGCAGCCTGGGCATCCCCGTGAACCACCTCATAGAGGGCTCCCAGAAGTGTGTGGCT 240	99.0%; Score 308.8; DB 25; Length 570; iimilarity 99.4%; Pred. No. 4.5e-53; longervative 0; Mismatches 2; Indels 0; Gaps 0; Arganacricaccoccrecragagacricacacccrearacrafter 1 arganacricaccccrearacaccicaccacccrearacaccicaccaccicaccaccicacci
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Search completed: September Job time: 149.781 secs
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Matches 310; Conserv
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P-PSDB; ABU10941.
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                    2003,
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Maximum DB
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Maximum Match 100%
Listing first 45 summaries
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seq length: 2000000000
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551
1 cggccggggaggcgggccggg.....gcgccccgagccccgcgcc 551
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Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                      Pending_Patents_NA_Main:*
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/cgn2_6/ptodata/2/pna/US081_cOMB.seq:*
/cgn2_6/ptodata/2/pna/US08_cOMB.seq:*
/cgn2_6/ptodata/2/pna/US08_COMB.seq:*
/cgn2_6/ptodata/2/pna/US080_COMB.seq:*
/cgn2_6/ptodata/2/pna/US090_COMB.seq:*
/cgn2_6/ptodata/2/pna/US090_COMB.seq:*
/cgn2_6/ptodata/2/pna/US090_COMB.seq:*
/cgn2_6/ptodata/2/pna/US092A.COMB.seq:*
/cgn2_6/ptodata/2/pna/US092A.COMB.seq:*
/cgn2_6/ptodata/2/pna/US093B_COMB.seq:*
/cgn2_6/ptodata/2/pna/US093B_COMB.seq:*
/cgn2_6/ptodata/2/pna/US093B_COMB.seq:*
/cgn2_6/ptodata/2/pna/US095A_COMB.seq:*
/cgn2_6/ptodata/2/pna/US095A_COMB.seq:*
/cgn2_6/ptodata/2/pna/US095A_COMB.seq:*
/cgn2_6/ptodata/2/pna/US095B_COMB.seq:*
/cgn2_6/ptodata/2/pna/US099B_COMB.seq:*
/cgn2_6/ptodata/2/pna/US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /ptodata/2/pna/PCTUS_COMB.seq:*
/ptodata/2/pna/PCTUS_COMB.seq.old:*
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44 // cgn2_6/ptodata/2/pna/US100A_COMB.seq; 45: // cgn2_6/ptodata/2/pna/US1010B_COMB.seq; 46: // cgn2_6/ptodata/2/pna/US1010B_COMB.seq; 47: // cgn2_6/ptodata/2/pna/US1010B_COMB.seq; 48: // cgn2_6/ptodata/2/pna/US1012B_COMB.seq; 49: // cgn2_6/ptodata/2/pna/US1012B_COMB.seq; 49: // cgn2_6/ptodata/2/pna/US1012B_COMB.seq; 50: // cgn2_6/ptodata/2/pna/US1012B_COMB.seq; 51: // cgn2_6/ptodata/2/pna/US1012B_COMB.seq; 52: // cgn2_6/ptodata/2/pna/US1012B_COMB.seq; 53: // cgn2_6/ptodata/2/pna/US1012B_COMB.seq; 53: // cgn2_6/ptodata/2/pna/US1012B_COMB.seq; 53: // cgn2_6/ptodata/2/pna/US1012B_COMB.seq; 54: // cgn2_6/ptodata/2/pna/US1012B_COMB.seq; 55: // cgn2_6/ptodata/2/pna/US1012B_COMB.seq; 56: // cgn2_6/ptodata/2/pna/US1012B_COMB.seq; 57: // cgn2_6/ptodata/2/pna/US1012B_COMB.seq; 57: // cgn2_6/ptodata/2/pna/US1012C_COMB.seq; 57: // cgn2_6/ptodata/2/pna/US1012C_COMB.seq; 57: // cgn2_6/ptodata/2/pna/US1012C_COMB.seq; 57: // cgn2_6/ptodata/2/pna/US1011_COMB.seq; 57: // cgn2_6/ptodata/2/pna/US1012_COMB.seq; 57: // cgn2_6/ptodata/2/pna/US1012_COMB.seq; 57: // cgn2_6/ptodata/2/pna/US1011_COMB.seq; 57: // cgn2_6/ptodata/2/pna/US1012_COMB.seq; 57: // cgn2_6/ptodata/2/pna/US1013_COMB.seq; 57: // cgn2_6/ptodata/2/pna/US1013_COMB.seq; 57: // cgn2_6/ptodata/2/pna/US1013_COMB.seq; 57: // cgn2_6/ptodata/2/pna/US1013_COMB.seq; 57:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

221	Result No.
509.2 509.2 488.6 486	Score
92.4 92.4 88.7 88.2	Query Match 1
547 547 66743 13386	Query Match Length DB ID
1 45 99 101	80
918	1
Sequence 19, Appl Sequence 19, Appl Sequence 995, App Sequence 87918, A	Description

60

Ν

120

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RESULT 1

PCT US02-05403-19

Sequence 19, Application PC/TUS0205403

GENERAL INFORMATION:

APPLICANT: Dana-Farber Cancer Institute, Inc.

APITE REFERENCE: 00530-094W01

CURRENT APPLICATION NUMBER: PCT/US02/05403

CURRENT APPLICATION NUMBER: E0270,973

PRIOR APPLICATION NUMBER: 60/270,973

PRIOR FILING DATE: 2001-02-23

PRIOR FILING DATE: 2001-02-23

PRIOR FILING DATE: 2001-02-23

PRIOR FILING DATE: 2001-02-23

PRIOR FILING DATE: 2001-01-25

NUMBER OF SEQ ID NOS: 32

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 19

LENGTH: 547

TYPE: DNA

DENGTH: DNA

DENGTH: DNA

DENGTH: 547
                                          ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 186
OTHER INFORMATION: n = C
PCT-USO2-05403-19
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Query Match
Best Local Similarity
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5 US-10-059-579-120
5 US-10-059-579-120
5 US-10-059-579-120
5 US-10-059-579-120
5 US-09-710-281-4055
3 US-09-770-175-80451
2 US-09-912-293-221180
7 US-09-912-293-221180
7 US-09-912-293-2914
4 US-10-027-632-196114
4 US-10-027-632-196114
5 US-09-770-175-4736
8 US-09-780-1838-5
5 US-09-16-387-5
5 US-09-16-387-11147
5 US-09-540-208-37787
8 US-09-18-387-387-6
10 US-09-19-383-366-4822
10 US-60-197-873-4822
10 US-60-197-873-48-2030
10 US-09-540-2174-1070
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US-09-762-130
US-10-242-799-18
US-10-426-002-18
US-09-927-796-27
US-09-927-796-27
US-10-210-858-27
US-10-211-858-27
US-10-211-848-27
US-10-211-849-27
US-10-210-938-407
US-09-941-992-407
US-09-989-293A-407
 Score 509.2; DB Pred. No. 1e-76;
                                                                                                                                                                                                                                                                                                                                                                                                                              ALIGNMENTS
             1;
           Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 297, App sequence 120, App sequence 120, App sequence 8431, Ap sequence 22118, Ap sequence 22118, Sequence 8, Appli sequence 8, Appli sequence 1, Appli sequence 6, Appli sequence 1070, Ap sequence 6, Appli sequence 1070, Ap sequence 6, Appli sequence 1070, Ap sequence 1070, Appli sequence 130, Appli sequence 130, Appli sequence 130, Appli sequence 27, Appli sequence 407, App sequence 407, App
                                                                                                                                        Sequence 19, Application US/10081817

SEQUENCANT: PO1YAK, KOZDELIA

APPLICANT: POTTET, Dale

APPLICANT: POTTET, Dale

APPLICANT: KTOP, Ian

TITLE OF INVENTION: HIN-1, A TUMOR SUPPRESSOR GENE

FILE REFERENCE: 00530-094001

CURRENT APPLICATION NUMBER: US/10/081,817

CURRENT FILING DATE: 2002-05-31

PRIOR APPLICATION NUMBER: 60/270,973

PRIOR FILING DATE: 2001-02-23

PRIOR FILING DATE: 2002-01-25

NUMBER OF SED ID NOS: 32

SOFTWARE: FastSED for Windows Version 4.0

SEQ ID NO 19

LENGTH: 547
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US-10-081-817-19
                                           ; OTHER INFORMATION: n = US-10-081-817-19
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Best Local Similarity
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                                                                     TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 186
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 92.4%;
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Score 509.2; DB Pred. No. 1e-76;
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             45;
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480

476

536

420

356 360 296

416

300

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; LENGTH: 66743
; TYPE: DNA
; ORGANISM: Human
US-60-449-155-995
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US-60-449-155-995
                                                                                                                                                                                                                                                                                                 Sequence 995, Application US/60449155

GENERAL INFORMATION:
APPLICANT; Keith, Tim
TITLE OF INVENTION: NUCLEOTIDE AND AMINO ACID SEQUENCES
TITLE OF INVENTION: RELATING TO RESPIRATORY DISEASES AND OBESITY
FILE REFERENCE: HUMO2-11P
CURRENT APPLICATION NUMBER: US/60/449,155
CURRENT ETLING DATE: 2003-02-20
NUMBER OF SEQ ID NOS: 1000
SOCTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 955
                                                                                                                                                           Query Match
Best Local S
Matches 529
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                                                                                                                                                        tch 88.7%;
al Similarity 95.8%;
529; Conservative
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                                                                                    CGGCCGGGAGGCCGGCAGGAGTGAGGCCTGATCGTCCCTGGCGCCTCCACCTCCCAGG
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                                       CGCAGAAGGCGCCCACGAGGACCCCCCAGTGCCCGACGTTTGCCCACGGTCTGGGATCAGAGG
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GCCCCCGCGCC 547
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                  CGCAGAAGGCGCCCACGAGGACCCCCAGTGCCCGACGTTGCCACGGTCTGGGATCAGAGG
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                                                                                                                                                        Score 488.6; DB 99;
Pred. No. 1.8e-73;
0; Mismatches 5;
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US-60-466-412-87918
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                                                                                                                                                                                                                                                                                                                                                                                    Sequence 87918, Application US/60466412

Sequence 87918, Application US/60466412

SEQUENCE INFORMATION:

APPLICANT: CARGILL, Michele
APPLICANT: LAKOUBOVA, Olga
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01466
CURRENT APPLICATION UNMEER: US/60/466,412
CURRENT APPLICATION APPLIC
                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 528
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                                                                                                                                                                         5551 CGCAGAAGGCCCCACGAGGACCCCCAGTGCCCGACGTTGCCACGGTCTGGGATCAGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            540
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                                                                                                                                        61 CGCAGAAGGCGCCCACGAGGACCCCCAGTGCCCGACGTTGCCACGGTCTGGGATCAGAGG
                                                                                                                                                                                                                                                                Similarity
                               GAGCGGAGCGGCAGGGCTTTCTCAGGAGCGCGGGCGAGGCCGGCGCTGGAGGGGCGAGG
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                                                                                                                                                                                                                                             88.2%; ilarity 95.7%; Conservative
                                                                                                                                                                                                                                                                                                                                    A,T,C or
                                                                                                                                                                                                                                           Score 486; DB 101;
Pred. No. 5.9e-73;
0; Mismatches 5;
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                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                Length 13386;
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                                                                  180
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QY 241 AGACCGCAAAGCGAAGGTGCGGGCCGGGGTGGGCCTCGCGGAGACAAAGGCCGGGCCTGC 300	Qy         181 CCCTCACCNGAGGGAAGCTCCCCTCACCCGGCCCAGCCCTGCAGGGGGGGG	Qy         121 CAGGGACCAGGGAGCCAGGAACTGCGCCGCCCCCGCCCCTGCCCTGGCGCGAGGGAAGCT 180           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Qy 61 CGCAGAAGGCGCCACGAGGACCCCCAGTGCCCGACGTTGCCACGGTCTGGGATCAGAGG 120	Oy     1 CGGCCGGGGAGGCGGCAGTGAGGCCTGATCGTCCCTGGCGCCTCCACCTCCCCAGG     60       IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Query Match 88.2%; Score 486; DB 75; Length 32768; Best Local Similarity 95.7%; Pred. No. 5.3e-73; Matches 528; Conservative 0; Mismatches 5; Indels 19; Gaps 2;	FEATURE: NAME/KEY: LOCATION: OTHER INFO S-60-213-178-	SEQ IU NO 29/ LENGTH: 32768 : TYPE: DNA : ORGANISM: Human	CURRENT APPLICATION NUMBER: US/60/213,178 CURRENT FILING DATE: 2000-06-22 NUMBER OF SEQ ID NOS: 1125 SOFTWARE: FastSEQ for Windows Version 4.0	TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES TITLE OF INVENTION: THEREOF FILE REFERENCE: CL000689	RESULT 5 US-60-213-178-297/c ; Sequence 297, Application US/60213178 ; GENERAL INFORMATION: ; APPLICANT: Hassley Ellen	Qy       540 AGCCCCCGCGCC 551         IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	QY       480 ACCGGGTATAÁGAAGCCTCGTGGCCTTGCCCGGGGCAGCAGCAGCTTCCCCGCGCGCCCCG 539	Qy 420 GAGCGGAGCGGCAGGGCTTTCTCAGGAGGGGGGGGGGGG	QY 360- GGGCACGGGCTTCCCAGGGCCCGCCGGCCGCCAGCAGGAAGTTGGCCAGGCACGGCCGT 419	301 5773	Db 5713 AGACCGCAAAGCTGCGGGCCGGGGTGGGCCTCGCGGAGACAAAGGCCGGGCCTGC 5772	5671 C
Qy 430 GGCAGGGCTTTCTCAGGAGCGGGGCGAGGCCGGGCGTGGAGGGGCGAGGACCGGGTATA 489	Qy 370 CTTCCCAGGGCCCGCCGGCCGCAGCAGCAGGAAGTTGGCCAGGGCACGGCCGTGAGCGGAGCG 429	Qy 310 AGGGCCCCAGCGCCTGCCAAGAGGAAGTCCTCGAGGCCCGGGCAGGGAAGGGGCACGGG 369	Qy 250 AGCGAAGGTGCGGGCCGGGGTGGGCCTGCCGGAGACAAAGGCCGGGCCTGCCT	Qy 190 GAGGGAAGCTCCCCTCACCCGGCCCAGCCCTGCAGGGGGGGCGCGTGGGGTCAGACCGCAA 249	Query Match 61.4%; Score 338.4; DB 45; Length 1794; Best Local Similarity 97.8%; Pred. No. 6.9e-48; Matches 354; Conservative 0; Mismatches 6; Indels 2; Gaps 1;	: misc_ 1: (359) #FORMATI	; SEO ID NO 120 ; LENGTH: 1794 ; TYPE: DNA ; ORGANISM: Homo sapiens	OR AP	TITLE OF INVENTION: ABERRANTLY METHYLATED GENES AS MARKERS OF BREAST MALIGNANCY; FILE REFERENCE: JHU1630-1 ; CURRENT APPLICATION NUMBER: US/10/059,579 ; CURRENT FILING DATE: 2003-02-03	APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE APPLICANT: SUKUMAR, Saraswati APPLICANT: EVRON, Ella APPLICANT: DOCLEY, William C. APPLICANT: DAVIDSON, Nancy APPLICANT: DAVIDSON, Nancy APPLICANT: DAVIDSON, Nancy	RESULT 6 US-10-059-579-120 ; Sequence 120, Application US/10059579 ; General Trongmation:	Db 3493 AGCCCCCGCGCC 3482		3613		Db 3733 CTGCTCTCAGAGGGCCCCAGCGCCTGCCAAGAAGAAGTCCTCGAGGCCCGGGCAAGGAAG 3674	Db 3793 AGACCGCAAAGCGAAGGTGCGGGCCTGGCGGGGTGGGGCCTGGCGGAGACAAAGGCCGGGCCTGC 3734  Qy 301 CT-CTCTCAGAGGGCCCCAGCGCCTGCCAAGAGGAAGTCCTCGAGGCCCGGGCAGGGAAG 359

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US-10-059-5/9A-120

Sequence 120, Application US/10059579A

GENERAL INFORMATION: HOPKINS UNIVERSITY SCHOOL OF MEDICINE
APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
APPLICANT: EUKON, Ella
APPLICANT: DOOLEY, William C.
APPLICANT: DAVIDSON, MARCY
TITLE OF INVENTION: ABERRAWTLY METHYLATED GENES AS MARKERS OF BREAST MALIGNANCY
TITLE OF INVENTION: ABERRAWTLY METHYLATED GENES AS MARKERS OF BREAST MALIGNANCY
TITLE REFERENCE: JUH1630-1
FILE REFERENCE: JUH1630-1
CURRENT APPLICATION NUMBER: US 09/771,357
PRIOR APPLICANTON UNMBER: US 09/771,357
PRIOR PRILING DATE: 2001-01-26
NUMBER OF SEQ ID NOS: 136
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 120
LEMOTH: 1794
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
LEMOTH: 1794
LEMOTH: 1795-179A-120
US-10-059-579A-120
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Best Local S
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1110 AGAAGCCTCGTGGCCTTGCCCGGGCAGCCCCAGGTTCCCCGCGCGCCCCGAGCCCCCGCG 1169
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                    CTTCCCACGGCCCCCCCCCCCAGCAGCAGGAAGTTGGCCAGGGCACGGCCGTGAGCGGAGCG 429
                                                                                                                                                                                                                                                   AGAAGCCTCGTGGCCTTGCCCGGGCAGCCGCAGGTTCCCCGCGCGCCCGAGCCCCGCG 549
                      CC 1171
                                                CC 551
                                                                                                                                                                                                                                                                                                                                                                                                                                61.4%;
ilarity 97.8%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 338.4; DB 45; Length 1794; pred. No. 6.9e-48; 0; Mismatches 6; Indels 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                929
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                                                                                                                                                     1109
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GENERAL INFORMATION:
APPLICANT: Gearing, David P.
APPLICANT: Gearing, David P.
APPLICANT: Holtzman, Douglas A.
APPLICANT: Holtzman, Douglas A.
APPLICANT: Holtzman, Douglas A.
APPLICANT: Holtzman, Douglas A.
APPLICANT: HOLTZMAN MOVEL NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1500.2058-001
FILE REFERENCE: 1500.2058-001
CURRENT APPLICATION NUMBER: US 60/170.175
CURRENT APPLICATION NUMBER: US 60/178,874
PRIOR FILING DATE: 2001-01-26
NUMBER OF SEO ID NOS: 8967
SOFTWARE: FASTSEQ for Windows Version 4.0
SEO ID NO 6431
LENGTH: 714
TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/164,254
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 5803
SOFTWARE: FESTSEQ for Windows Version 4.0
SEQ ID NO 4055
LENGTH: 627
TYPEN - NAN
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US-09-770-175-8431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Hunter, John J.
APPLICANT: Shyjan, Andrew W.
APPLICANT: Stodal, Hilde
APPLICANT: Stodal, Hilde
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES.
TITLE OF INVENTION: THEREFOR
TITLE OF INVENTION: THEREFOR
TITLE REFERENCE: 1600.2036-001
CURRENT APPLICATION NUMBER: US/09/710,281
CURRENT FILING DATE: 2000-11-10
CURRENT FILING DATE: 2000-11-10
                                                                                                                                                                                                                    ; ORGANISM: Homo sapiens US-09-770-175-8431
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Best Local Similarity 96.6
Matches 173; Conservative
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Best Local S
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                                                                                                   493
                                                                                                                                                                173;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGGGCTTTCTCAGGAGCGCGGGCGAGGCCGGCGCGTGGAGGGGCGAGGACCGGGTATAAGA 492
                                                                                                                                                                            Similarity
                                           AGGGCTTTCTCAGGAGCGCGGGCGAGGCCGGCGCTGGAGGGGCGAGGACCGGGTATAAGA 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Application US/09710281
Conservative
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                                                                                                                                                                               30.7%;
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pred. No. 3e-19;
0; Mismatches 6;
                                                                                                                                                                     0;
                                                                                                                                                                 Score 169.4; DB 33;
Pred. No. 3e-19;
0; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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RESULT 10 US-08-790-774-9245

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Sequence 221180, Application US/09912293
GENERAL INFORMATION:
APPLICANT: ROSEN, et. al.
TITLE OF INVENTION: Human Genes, Sequences,
EILE REFERENCE: PO-100
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CURRENT APPLICATION NUMBER: US/09/912,293 CURRENT FILING DATE: 2001-07-26 PRIOR APPLICATION NUMBER: 08/103,744 PRIOR FILING DATE: 1993-08-09 PRIOR APPLICATION NUMBER: 09/249,651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/790,7:
FILING DATE: JAN-30-1997
CLASSIFICATION: |536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/010,822
FILING DATE: JAN-30-1996
ATTORNEY/AGENT INFORMATION:
NAME: MICHALE M. WALLS
REGISTRATION NUMBER: P-43,975
REGISTRATION INFORMATION:
TELECHMUNICATION INFORMATION:
TELECHMUNICATION INFORMATION:
TELECHMUNICATION INFORMATION:
TELECHMUNICATION INFORMATION:
TELECHMUNICATION INFORMATION:
TELECHMUNICATION | 309-8504
                                                                                                                                                                                                                                                                                                                                                                                          434 GGGCTTTCTCAGGAGCGCGGGCGAGGCCGGCGCTGGAGGGGCGAGGACCGGGTATAAGAA 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             374 CCAGGGCCGGCGGCGCAGCAGGAAGTTGGCCAGGGCACGGCCGTGAGCGGAGCGGGCA 433
                                                                                                                                                                                                                                                                                   CANGGNCCGCCGCCGCAGCAGCAGGAAGTTGGCCAGGGCACGGCCGTGAGCGGNNGGGNCA 68
                                                                                                                                                                                                                                                                                                                                                                     GGGGNTTCTCAGNNNCGCGGGCGAGGCCGGCGTNGAGGGGCGAGGACCGGGTATAAGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Human Genome Sciences,
9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Diskette, 3.50 inch, 1.4Mb
HP Vectra 486/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JAN-30-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human Genes, Sequences, and Expression Products 9715
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 160.8; DB 12;
Pred. No. 9.7e-18;
D; Mismatches 16;
                                                                                                                       and Expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 12;
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                                                                                                                         Products
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PRIOR APPLICATION NUMBER: 08/215
PRIOR APPLICATION NUMBER: 08/221,623
PRIOR APPLICATION NUMBER: 08/221,623
PRIOR APPLICATION NUMBER: 08/220,691
PRIOR FILING DATE: 1994-03-31
PRIOR FILING DATE: 1994-03-31
PRIOR FILING DATE: 1994-03-31
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 09/741,830
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEO ID NOS: 244538
SEO ID NO 221180
PRIOR FILING DATE: 2001-03-21
REMAINING PRIOR APPLICATION NUMBER: 09/813,155
PRIOR FILING DATE: 2001-03-21
REMAINING PRIOR APPLICATION MARKET NUMBER OF SEO ID NOS: 244538
                  ; LOCATION: (200)..(200); OTHER INFORMATION: n is US-09-912-293-221180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: 08/104,507
PRIOR FILING DATE: 1993-08-09
PRIOR APPLICATION NUMBER: 08/196,363
PRIOR FILING DATE: 1994-02-15
PRIOR APPLICATION NUMBER: 09/859,490
PRIOR FILING DATE: 2001-05-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
LOCATION: (12)..(12)
OTHER INFORMATION: n is
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OTHER INFORMATION: n is
                                                                                                                     LOCATION: (185)..(185)
OTHER INFORMATION: n is
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LOCATION: (155)..(155)
OTHER INFORMATION: n is
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LOCATION: (142)..(142)
OTHER INFORMATION: n is
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LOCATION: (103)..(103)
COTHER INFORMATION: n is
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OTHER INFORMATION: n is
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OTHER INFORMATION: n is
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                                                                                NAME/KEY: misc_feature
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LOCATION: (61)..(62)
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LOCATION: (15)..(15)
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                                                                                                                                              NAME/KEY: misc_feature
LOCATION: (185)..(185)
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                                                                                                                                                                                                                                                                                                                                                                                                                                   TEATURE:
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LOCATION: (66)..(66)
                                       equal to a,t,g, or
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9

Matches Query Match

Local

tch | 29.2%; al Similarity | 91.0%; 162; Conservative

US-08-790-774-9245

TELEFAX: (301) 309-8312
INFORMATION FOR SED ID NO: 92.
SEQUENCE CHARACTERISTICS:
LENGTH: 210 base, pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear

OPERATING SYSTEM: MSDO SOFTWARE: ASCII Text CURRENT APPLICATION DATA:

COMPUTER READABLE FORM: MEDIUM TYPE: Diskett

COUNTRY:

20850

CITY: Rockville STREET:

Maryland

USA

CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Gen TITLE OF INVENTION: NUMBER OF SEQUENCES:

A. Rosen

밁 ρy

129

494

RESULT 11 US-09-912-293-221180

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GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/09/634,306B
CURRENT FILING DATE: 2002-202-21
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/166,358
PRIOR APPLICATION NUMBER: US 60/166,358
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION 
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US-09-634-306B-196114/c
; Sequence 196114, Application US/09634306B
; GENERAL INFORMATION:
DEADLY DEADLY
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US-09-634-306B-196114
RESULT 13
US-10-027-632-196114/c
; Sequence 196114, Application US/10027632
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Best Local (
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 CGCAGAAGGCGCCCACGAGGACCCCCAGTGCCCGACGTTGCCACGGTCTGGGATCAGAGG
                                                                                                                                                                                                                                                                                              180 TCCCTCACCNG 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 143.6; DB 27; Length 533; Pred. No. 7.1e-15; O; Mismatches 5; Indels 5;
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RESULT 14

US-09-770-175-4736

US-09-770-175-4736

Sequence 4736, Application US/09770175

Sequence 4736, Application US/09770175

GENERAL INFORMATION:
APPLICANT: HOILZMAN, David P.
APPLICANT: HOILZMAN, DOUGLAS A.
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREOR
FILE REFERENCE: 1600.2058-001
CURRENT APPLICATION UNMBER: US/09/770,175
CURRENT APPLICATION NUMBER: US 60/178,874
PRIOR APPLICATION NUMBER: US 60/178,874
PRIOR FILING DATE: 2000-01-28
NUMBER OF SEQ ID NOS: 8967
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 4736
LENGTH: 624
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(624)
OTHER INFORMATION: n = A,T,C or G
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APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/195,218
PRIOR APPLICATION NUMBER: US 60/195,363
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,363
PRIOR APPLICATION NUMBER: US 60/185,363
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/166,358
PRIOR APPLICATION NUMBER: US 60/166,358
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
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US-10-027-632-196114
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APPLICANT: ADDOTT LAUGH CALLED APPLICANT: COLDITIT, Tracey L.

APPLICANT: RUSSELL, JOAN C.

ITILE OF INVENTION: REAGENTS AND METHODS USEFUL FOR

ITILE OF INVENTION: DETECTING DISEASES OF THE REPRODUCTIVE TISSUES

FILE REFERENCE: 5972.U$.96

CURRENT APPLICATION NUMBER: DCT/US01/09339

CURRENT FILING DATE: 2001-03-22

PRIOR FILING DATE: 1999-12-20

PRIOR APPLICATION NUMBER: US 09/467,602

PRIOR APPLICATION NUMBER: US 09/215,818

PRIOR APPLICATION NUMBER: US 08/912,76

PRIOR APPLICATION NUMBER: US 08/912,76

PRIOR APPLICATION NUMBER: US 08/912,76

PRIOR APPLICATION NUMBER: US 08/597,105

PRIOR APPLICATION NUMBER: US 08/597,105

PRIOR FILING DATE: 1996-08-19

NUMBER OF ESO ID NOS: 12

SOPTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                         PEATURE:

NAME/KEY: misc_feature

LOCATION: (17)...(17)

OTHER INFORMATION: n = a or g or c or t/u, unknown or other at

OTHER INFORMATION: position 17

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PCT-US01-09339-8
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Best Local Similarity 99.2%;
Matches 120; Conservative
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Best Local
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ORGANISM: Homo sapiens
                                                                                                                   127
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                            551 C 551
                                                        al Similarity
150; Conserv
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Pred. No. 1.8e-11;
0; Mismatches 9; Indels 3;
                                                                                                                                                                                Score 120; DB 1;
Pred. No. 6.9e-11;
0; Mismatches 1
                                                                                                                                                                                1; Indels
                                                                                                                                                                                                            Length 562;
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Search completed: September 20, 2003, 03:12:36 Job time: 3508.06 secs

Run

Title: Perfect score: Sequence:

Scoring table:

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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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length: 2000000000
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1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq:*

2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq:*

3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq:*

4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:*

5: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:*

6: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:*

6: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:*

7: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:*
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Match Length
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  S US-10-081-817A-19
PCT-US33-21379-7
S US-10-487-610-1981
US-60-487-610-1981
US-60-487-610-1984
US-60-487-610-1984
US-60-487-610-1984
S US-60-485-114A-2674
S US-60-495-114-16671
US-60-495-114-16855
PCT-US33-1251-14A-26227
US-60-495-114-16806
PCT-US32-36071A-58
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Compugen Ltd
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        Sequence 1, Appli
Sequence 3, Appli
Sequence 33423, A
Sequence 19981, A
Sequence 12047, Ap
Sequence 2674, Ap
Sequence 1677, Ap
Sequence 16875, A
Sequence 16875, A
Sequence 16805, Appl
Sequence 26227, Ap
Sequence 16805, Appl
Sequence 16323, A
Sequence 1437, Ap
Sequence 1437, Appl
Sequence 15207, A
Sequence 19824, A
Sequence 1591, A
Sequence 1591, A
Sequence 1591, A
Sequence 1592, A
Sequence 1592, A
Sequence 1592, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Description
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Sequence 19, Application US/10081817A
Sequence 19, Application US/10081817A
Sequence 19, Application US/10081817A
REPLICANT: POLYAK, Kornelia
APPLICANT: STOTAL: Dale
APPLICANT: STOTAL: Dale
APPLICANT: STOP, IBA
APPLICANT: KTOP, IBA
APPLICANT: KTOP, IBA
TITLE OF INVENTION: HIN-1, A TUMOR SUPPRESSOR GEN
TITLE REFERENCE: 00530-094001
FILE REFERENCE: 00530-094001
FILE REPLICATION UNMBER: US 60/270,973
PRIOR APPLICATION UNMBER: US 60/270,973
PRIOR APPLICATION UNMBER: US 60/351,908
PRIOR APPLICATION UNMBER: US 60/351,908
PRIOR FILING DATE: 2002-01-25
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FEASUSED for Windows Version 4.0
SEQ ID NO 19
SEQ ID NO 19
SEQ ID NO 19
LENGTH: 551
LENGTH: 551
LENGTH: 551
COCATION: 189 centure
LOCATION: 189 
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US-10-081-817A-19
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Best Local Similarity
Matches 551; Conserv
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Conservative
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US-10-425-114A-31613
US-10-425-114A-31613
US-10-425-114A-26232
US-00-487-610-19371
US-60-485-114-16973
US-60-485-114-16936
US-60-495-114-16936
US-60-495-114-15371
US-60-487-610-19525
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Sequence 31612, A
Sequence 31613, A
Sequence 26227, A
Sequence 26232, A
Sequence 19371, A
Sequence 19372, A
Sequence 16932, A
Sequence 16948, A
Sequence 23195, A
Sequence 23195, A
Sequence 589, App
Sequence 589, App
Sequence 11371, A
Sequence 19525, A
Sequence 19525, A
Sequence 11443, A
Sequence 11443, A
Sequence 11483, A
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CURRENT APPLICATION NUMBER: PCT/US03/21379
CURRENT FILING DATE: |2003-07-09
PRIOR APPLICATION NUMBER: US 60/394,845
PRIOR FILING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: US 60/410,986
PRIOR FILING DATE: 2002-09-16
NUMBER OF SEQ ID NOS: 1100
SOFTWARE: PATENTIN OS: 1100
SOFTWARE: PATENTIN VETSION 3.2
SEQ ID NO 7
SEQ ID NO 1133
TYPE: DNA
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PCT-US03-21379-7/C
; Sequence 7, Application PC/TUS0321379
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVESTION: MCHKS AS MODIFIERS OF THE CHK1 PATHWAY AND METHODS OF
; FILE REFERENCE: EX03-047C-PC
; FILE REFERENCE: EX03-047C-PC
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Best Local Similarity | 49.8%;
Matches 160; Conservative
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                         CGCGCCCGAGCCCCCGCGCC 551
                                                                         GGGGCGAGGACCGGGTATAAGAAGCCTCGTGGCCTTGCCCGGGGCAGCCGCAGGTTCCCCG
                                                                                                                     CACGGCCGTGAĞCGGAGGCGGCAGGGCTTCTCTCAGGAGCGCGGGGCGAGGCCGGGGCTGGA
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                                                     CCCCCCGGGCGCTCCGGGTCCGCCGCGCAGGTCGGC--CAGGATGCTGGCGGCCAGCA
                                                                                                                                                                                                               GGGCACGGGCTTCCCAGGGCCCGCCGGCCGCAGCAGGAAGTTGGCCAGGGCACGGCCGTG
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Pred. No. 0.064;
0; Mismatches 159;
92
                                                                                                                                                                                                                                                                                                                                                Length 1133;
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US-10-425-114A-33423/c

US-10-425-114A-33423/c

Sequence 33423, Application US/10425114A

EGRERAL INFORMATION:

APPLICANT: Liu, Jingdong

APPLICANT: Liu, Jingdong

APPLICANT: Kovalic, David K.

APPLICANT: Kovalic, David K.

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53313)B

CURRENT APPLICATION NUMBER: US/10/425,114A

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NO 33423

LENGTH: 1431

TYPE: DNA

ORGANISM: Zea mays

FEATURE: TO THE ACTION OF TH
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nes 244;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           679 GGCGGCGTCCTCGAGCGCGCGCAGCAGCGCCTCCGCCTTGGCCTTCCCCCGGGGGCTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68 GGCGCCCACGAGGACCCCCAGTGCCCGACGTTGCCCACGGTCTGGGATCAGAGGCAGGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 GGAGGCGGCCGGGAGTGAAGGCCTGATCGTCCCTGGCGCCCTCCACCTCCCCAGGGGCGCAGAA 67
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                                                CGCGCC 551
                                                                                                                                                                                                                                       AGCGGGCAGGGCTTTCTCAGGAGCGCGGGGGGGAGGGCGAGGGCGAGGACCGGG 485
                                                                                                                                                                                                                                                                                                               GGCTTCCCAGGGCCCGCCCGCCGCCGCCAGGAGGTTGGCCAGGGCACGGCCGTGAGCGG 425
                                                                                                                                                                                                                                                                                                                                                                                                                         GETGGCGTCCTCCACGACGCCGCGCGCGCGCGTCCGTGAGCACGAGCGCGAAGAGCGCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGAGGGCCCCAGCGCCTGCCAAGAGGAAGTCCTCGAGGCCCGGGCAGGGAAGGGGGCACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGCCGCGGCGGCCTCCCCGCCGGCCACGACGAGGTTGAGCAGCGCGGCAGCGGCGTTCTC
                                                                                                   GGAGACCCAGCGGAAGGCCTCGAGGCTCTCGGCGCACCCGGCCACCTGCGCGACCACGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCGCGCCCTGGGCGGCAGCGCCCCCAGACTCGACGAGGTCGAGGAGGATGCGCACCCC
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134
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Pred. No. 0.066;
0; Mismatches 300; Indels 2
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RESULT 4 US-60-487-610-19981 ; Sequence 19981, Application US/60487610

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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(147727)
; OTHER INFORMATION: n = I
US-60-487-610-19981
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ORGANISM: Homo sapiens
US-60-487-610-1384
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APPLICANT: CARGILL, Michele
APPLICANT: HUANG, Hongjin
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,
TITLE OF INVENTION: METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001469
CURRENT FILMG DATE: 2003-07-17
CURRENT FILMG DATE: 2003-07-17
NUMBER OF SEQ ID NOS: 97101
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 19981
LENGTH: 147727
TYPET- NA
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Best Local S
Matches 184
                     Sequence 1384, Application US/60487610

SEQUENCE 1387, Application US/60487610

SERVERAL INFORMATION:

APPLICANT: LAVELLY, Michele
APPLICANT: HUANG, HONGJİN

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001469

FULE REFERENCE: CL001469

CURRENT APPLICATION NUMBER: US/60/487,610

CURRENT APPLICATION NUMBER: US/60/487,610

CURRENT FILING DATE: 2003-07-17

NUMBER OF SEQ ID NOS: 97101

SOFTWARE: FRAETSEQ for Windows Version 4.0

SEQ ID NO 1384

LENGTH: 4989

TYPE: DNA. Homo saniens
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al Similarity 47.8%;
184; Conservative
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                                                                                                                                                                                                                                                                                                                      CCCCGCGCGCCCCCGAGCCCCCCGCGC
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Pred. No. 0.13;
); Mismatches 197;
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                                                                                                                                                                                                                                                                                                6378
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                      331
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RESULT 6

US-60-485-450-12047/c

Sequence 12047, Application US/60485450

EGENERAL INFORMATION: Michele

APPLICANT: CHANG, Sheng-Yung

APPLICANT: CHANG, Sheng-Yung

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

TITLE OF INVENTION: TRESPONSE TO INTERFERON TREATMENT IN HEPATITIS C

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: VIUGS-INFECTED SUBJECTS, METHODS OF DETECTION AND

TITLE OF INVENTION UNDER: US/60/485,450

CURRENT APPLICATION NUMBER: US/60/485,450

CURRENT FILING DATE: 2003-07-09

NUMBER OF SEQ ID NOS: 47859

SOFTMARE: FastSEQ for Windows Version 4.0

SEQ ID NO 12047

LENGTH: 16525

TYPE: DNA

COGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 182; Conserv
                                                                                                                                                                                                                              Query Match 9.3
Best Local Similarity 48.8
Matches 163; Conservative
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                                              5981 CCCGGGCTCGGGCCGCCCCCCGGCCGGCCGGGCTGGCCCGCGCGCGAACGCATGGCCCG
                                                                                                                                                                 358 CACACAATAGCGGCGCGCGC
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                                                                                                                            CCAGCCCTGCAGGGGGGCGCGTGGGGTCAGACCGCAAAGCGAAGGTGCGGGGCCGGGGTG
                                                                Conservative
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Pred. No. 0.093;
0; Mismatches 194;
                                                                                                                                                                                                                              Score 50.6; DB 7;
Pred. No. 0.23;
0; Mismatches 170;
                                                                                                                                                                                                                                 170;
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RESULT 7
US-10-425-114A-2674/c
US-mence 2674, Application US/10425114A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(5313)8 CURRENT APPLICATION NUMBER: US/10/425,114A CURRENT FILING DATE: 2003-04-28 NUMBER OF SEQ ID NOS: 73128 SEQ ID NO 2674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 9.0%;
Best Local Similarity 45.0%;
Matches 224; Conservative
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GENERAL INFORMATION:
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APPLICANT:
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ORGANISM: Zea mays
FEATURE:
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                                                                                                   GAGGCCGGCGCTGGAGGGGCGAGGACCGGGTATAAGAAGCCTCGTGGCCTTGCCCGGGCA 515
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                                                                 GCGGCGCAGCGCGGCCAGGAGCCTGGGCACGAGCGGCGCGACGGCGTCCCCGCGGGTG
                                                                                                                                                                             GGAAGTTGGCCAGGGCACGGCCGTGAGCGGAGCGGGCAGGGCTTTCTCAGGAGCGCGGGC
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Pred. No. 0.25;
0; Mismatches 273;
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US-09-897-516A-4197/c
US-09-897-516A-4197/c
Application
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FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(1215)
OTHER INFORMATION: unsure at all n locations
US-09-897-516A-4197
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Huesing, Joseph E.
APPLICANT: Malvar, Thomas M.
APPLICANT: Stater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Spiridonov, Sergei
TITLE OF INVENTION: Xenorhabdus sp. Genome Serfile Reference: 38-21 (51847) B
CURRENT APPLICATION NUMBER: US/09/897,516A
CURRENT APPLICATION NUMBER: US 60/215,161
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
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PCT-US03-26780-822/c
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SEQUENCE 822, Application PC/TUS0326780

SEQUENCE 822, Application PC/TUS0326780

SEQUENCE 822, Application PC/TUS0326780

GENERAL INFORMATION: THERAPEUTICS, INC.

TITLE OF INVENTION: HUMAN POLYPEPTIDES ENCODED BY POLYNUCLEOTIDES AND METHODS OF TITLE OF INVENTION: HUMAN POLYPEPTIDES ENCODED BY POLYNUCLEOTIDES AND METHODS OF TITLE REFERENCE: 08940.0014-00304

CURRENT APPLICATION NUMBER: PCT/US03/26780

CURRENT FILING DATE: 2003-08-28

PRIOR APPLICATION NUMBER: 60/406,519

PRIOR APPLICATION NUMBER: 60/406,579

PRIOR APPLICATION NUMBER: 60/406,555

PRIOR APPLICATION NUMBER: 60/406,655

PRIOR APPLICATION NUMBER: 60/406,655

PRIOR FILING DATE: 2002-08-29

PRIOR PRIOR PRIOR DATE: 2002-08-29

PRIOR PRIOR PRIOR DATE: 2002-08-29

PRIOR PRIOR PRIOR DATE: 2002-08-29
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SEQ ID NO 4197
LENGTH: 1215
TYPE: DNA
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Best Local
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APPLICANT: Goldman, Barry
APPLICANT: Hinkle, Gregory
APPLICANT: Huesing, Joseph
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Pred. No. 0.25;
0; Mismatches 132;
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PRIOR APPLICATION NUMBER: 60/406,642
PRIOR FILING DATE: 2002-08-29
PRIOR FILING DATE: 2002-08-29
PRIOR FILING DATE: 2002-08-29
PRIOR PRIOR PLING DATE: 2002-08-29
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: 60/406,576
PRIOR APPLICATION NUMBER: 60/406,646
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: 60/406,666
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: 60/406,666
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: 60/406,653
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: 60/406,653
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: 60/406,653
PRIOR FILING DATE: 2002-08-29
PRIOR PRIOR FILING DATE: 3002-08-29
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                                        RESULT 10
US-60-495-114-16671
Sequence 16671, Application US/60495114
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
TITLE OF INVENTION: DOLLMORPHISMS IN NUCLEIC ACID MOLECULES
TITLE OF INVENTION: ENCODING HUMAN PROTEASE PROTEINS, METHODS OF DETECTION INTILE OF INVENTION: USES THEREOF
TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION: USES THEREOF
CURRENT APPLICATION NUMBER: US/60/495,114
CURRENT FILING DATE: 2003-08-15
NUMBER OF SEQ ID NOS: 91238
SOFTWARE: FastSEQ for Windows Version 4.0
ENCTH: 65518
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Best Local Similarity
Matches 189; Conserv
ORGANISM: Homo sapiens
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Pred. No. 0.31;
0; Mismatches 214;
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SEQUENCE 1685, Application US/60495114

SEQUENCE 1685, Application US/60495114

SEQUENCE 1685, Application US/60495114

APPLICANT: CARGILL, Michele
APPLICANT: CARGILL, Michele
TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
TITLE OF INVENTION: ENCODING HUMAN PROTEASE PROTEINS, METHODS OF I
TITLE OF INVENTION: USES THEREOF

FILE REFERENCE: CL001480
CURRENT APPLICATION NUMBER US/60/495,114
CURRENT FILING DATE: 2003-08-15
NUMBER OF SEO ID NOS: 91238
SOFTMARE: PASTSEQ FOR WINDOWS VETSION 4.0
SEO ID NO 16855
LENGTH: 121612
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(65518)
OTHER INFORMATION: n =
US-60-495-114-16671
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US-60-495-114-16855
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                                                                                                                                                                                                                                                                                                            FEATURE:

NAME/KEY: misc_feature
LOCATION: (1)...(121612)
THER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism
US-60-495-114-16855
                                                                                   Qy
                                                                                                                      В
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Best Local S
Matches 107
                    δδ
                                                           Вþ
                                                                                                                                                                                                                                             Query Match 8.9%;
Best Local Similarity 52.5%;
Matches 107; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64441 GGAGGAGGCCGGGTACCCGGGGTGCGGGCGCGCGGGAGGAAGGCGGGGCCTCGGGCGAG
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                                                                                                                                                                                    al Similarity 52.5
107; Conservative
                                                                                                                                                                                                         339 CTCGAGGCCCGGGCAGGAAGGGGGCCACGGCCTTCCCAGGGCCCGCCGCCGCAGGAGGA 398
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                                                                                                                       GGAGGAGGCCGGGTACCCGGGGTGCGGCGCGCGCGGGAGGAAGGCGGGGCCTCGGGCGAG
                                                                                                                                                 AGTTGGCCAGGGCACGGCCTGAGCGGAGCGGGCAGGGCTTTCTCAGGAGCGCGGGCGAG
ceceeeccececccceeecc 5992
                             GCAGGTTCCCCGCGCGCGCCCGAGC 542
                                                            GCCGGCGCTGGAGGGCCGAGGACCGGGTATAAGAAGCCTCGTGGCCTTGCCCCGGGCAGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 48.8; DB 7; Length 65518; pred. No. 0.61; 0; Mismatches 97; Indels 0;
                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                   Score 48.8; DB 7;
Pred. No. 0.66;
0; Mismatches 97;
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RESULT 12 PCT-US03-11231-193/c

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RESULT 13

US-10-425-114A-26227
; Sequence 26227, Application U;
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K
; APPLICANT: Screen, Steven E
                                 ; OTHER INFORMATION: Clone US-10-425-114A-26227
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                                                                    APPLICANT: Zhou, Yihua

APPLICANT: Kovalic, David K.

APPLICANT: Screen, Steven E

APPLICANT: Screen, Steven E

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleake Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53313)B

CURRENT APPLICATION NUMBER: US/10/425,114A

CURRENT APPLICATION NUMBER: US/10/425,114A

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEO ID NOS: 7312B

SEO ID NO 2627

LENGTH: 2463

TYPE: DNA

ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: DNA
; ORGANISM: HSV2
PCT-US03-11231-193
      Query Match
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Best Local Similarity
Matches 157; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Hosken, Nancy A.
APPLICANT: Hosken, Nancy A.
APPLICANT: Parsons, Joseph M.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
FILE REFERENCE: 210121,53801.PC
CURRENT APPLICATION NUMBER: PCT/US03/11231
CURRENT FILING DATE: 2003-04-09
NUMBER OF SEQ ID NOS: 267
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 193
LENGTH: 3957
TWORP: Nan
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                                                            FEATURE:
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APPLICANT: Day,
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     8.6%;
                                               ID:
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                                           LIB4118-190-H1_FLI
   Score 47.6;
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   DB
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 Length
2463;
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TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated: TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated: FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114A
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO SE322
TYPE: DUA
ORGANTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 26232, Application US
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Clone ID: LIB4119-019-H6_FLI US-10-425-114A-26232
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US-10-425-114A-26232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                 243 TTCGCTCCGGGCTCGGAGCCTCCGAGGCCAGGCCAGTCCCCTGAGCCTTCGCCGGCCCCG
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140; Conserv
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CGGCCCTGTCCGACGGCCCCAGGCTGGCCCCGGCTCCCGGCCCAGGCTCC
                               CGCCTGATGGACCTGGCTCCGGGCGGGCCCGGGCCCCGGGCCCCCTTGGGCC
                                                                                                      TTTCTCAGGAGCGCGGGGGAGGCCGGCGCGCGGGGAGGACCGGGTATAAGAAGCCT
                                                                                                                                         GGCCCGCCGCCAGCAGGAAGTTGGCCAGGGCACGGCCGTGAGCGGAGCGGGCAGGGC
                                                                                                                                                                                                              GGTCCGGGCCGTCGCGGGGGCCCGCGAGCTGGCCCGGCAGATCCGGGCGCGCTACGAG
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ilarity 47.6%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                          0; Mismatches 154;
                                                                                                                                                                                                                                                                                                                                                                          Score 47.6; DB Pred. No. 0.69;
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0; Mismatches
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536
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US-60-495-114-16806/c
US-60-495-114-16806/c
US-60-495-114-16806, Application US/60495114

Sequence 16806, Application US/60495114

GENERAL INFORMATION:
GENERAL INFORMATION:
HICKORIAN HICKORY IN NUCLEIC ACID MOLECULES
TITLE OF INVENTION: DELYMORPHISMS IN NUCLEIC ACID MOLECULES
TITLE OF INVENTION: DELYMORPHISMS IN NUCLEIC ACID MOLECULES
TITLE OF INVENTION:
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CL001480
CURRENT APPLICATION UMBER: US/60/495,114
CURRENT FLING DATE: 2003-08-15
NUMBER OF SEQ ID NOS: 91238
SOUTHWARD: FastSEQ for Windows Version 4.0
SEQ ID NO 16806
LENGTH: 27991
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
RAME/KEY: misc_feature
LOCATION: (1)...(27991)
COTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism
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Search completed: September 20, 2003, 03:15:44
Job time: 116.54 secs
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Best Local Similarity 49.5%;
Matches 147; Conservative
                                                                              25458
                                                                                                                                                                                                                                                                                                                                                    264 CCGGGGTGGGCCTCGCGGAGACAAAGGCCGGGCCTGCCTCTCAGAGGGCCCCAGCGCC 323
                                                                                                                                                                                                                                                                                                                                                                                                                                         204 TCACCCGGCCCAGCCCTGCAGGGGGGGGGGCGCGGGGGTCAGACCGCAAAGCGAAGGTGCGGG 263
                                                                                                                                                                                                                                                CGCCCTCGCAGACGCCGCGCGCTCTTCCGGGGCCCTGGCGGGCCCGGGGACCGAGGGGGCC 25399
                                                                                                                                                                                                                                                                                    TGCCAAGAGGAAGTCCTCGAGGCCCGGGCAGGGAAGGGGGCACGGGCTTCCCAGGGCCCG 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 46.6; DB 7; Length 27991;
Pred. No. 1.5;
0; Mismatches 149; Indels 1;
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Service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the servic The state of the s 

B1769722 603055021
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B0067622 AGENCOURT
BM921624 AGENCOURT
BM921624 AGENCOURT
BM927779 UI-CF-ENI
A1665860 tt90f9.x
B1819014 603033130
B1819014 603033130
B1819014 603032283
B1819014 603032283
B1819795 603042303
B1819795 603042586
AI333740 qp98f05.x
AI187341 qe26d06.x
B1821791 603055866
AI333740 qp98f05.x
B1821791 603055866
AI33740 qp98f05.x
B1821212 603039244
B18181834 603033053
AI74557 wc34e01.x
BM921212 UI-CF-ENI
BM921212 UI-CF-ENI
BM921212 UI-CF-ENI
BM921212 UI-CF-ENI
BM921212 UI-CF-ENI
BM921212 UI-CF-ENI
BM92121 UI-CF-ENI
BM921307 UI-CF-ENI
BM92045 UI-CF-ENI
BM92049 UI-CF-ENI
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       Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs r@mail.nlh.gov
Tissue procurement: Life Technologies, Inc.
Tissue procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
cDNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAMI2785 row: j column: 07
High quality sequence stop: 474.
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Euteleostomi;
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Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: cgapbs remail.nih gov

Tissue Procurement: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can
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Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 473)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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5', mRNA sequence.
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                                                                               REFERENCE
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SOURCE
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BM977626/c
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Query Match
Best Local Similarity
Matches 310; Conserv
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                                                      Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 490)
Bonaldo,M.F., Lennon,G. and Soares,M.B.

Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9),
97044477
                                                                                                                                                                                                                                                                                                                                                                                                   BM977626

490 bp mRNA linear UI-CF-EN1-aef-o-13-0-UI.51 UI-CF-EN1 Homo sapiens UI-CE-EN1-aef-o-13-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                            BM977626.1 GI:19596235
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ilarity 99.4%;
Conservative
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Location/Qualifiers
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Pred. No. 1.20
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1.2e-50;
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                                                                                                                                                                                                                                                   Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com) or from Open Biosystems
(www.openbiosystems.com).
The following repetitive elements were found in this cDNA
sequence: 459-484, >GC_Tich#Low_complexity
Seq primer: M13 FORWARD
POLYA-Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             University of Iowa Med Labs, Iowa City, IA 52242, USA Tel: 319 356 4866 Fax: 319 356 7171
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GAGCTGGGTCCCCAGGCCGTGGGGGCCCTGAAGGCCCTGAAGGCCCTGCTGGGGGCCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /uev_seq= Audut
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modified polylinker; Site_1: EcoR I; Site_2: Not I;
modified polylinker; Site_1: EcoR I; Site_2: Not I;

UI-CF_ENI is a normalized cONA library containing the
following tissue(s): Primary Lung Cystic Fibrosis
Epithelial Cells. The library was constructed according to
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
Bonaldo, Lennon and 
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ilarity 99.4%;
Conservative
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154 c 175 g
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Pred. No. 1.2e-50;
D; Mismatches 2;
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VERSION
KEYWORDS
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AUTHORS
TITLE
JOURNAL
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Matches 310;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

El (bases 1 to 496)

National Institutes of Health, Mammalian Gene Collection (MGC)

Email: cgapbs remail.nih.gov

Tissue Procurement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://dmax.ac.lln.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301 ACAGTGTTTGGC
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BI818715
BI818715.1 GI:15930265
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603037535F1 NIH_MGC_115 Homo
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Plate: LLAMIL1445 row: e column: 09
High quality sequence stop: 471.
Location/Qualifiers
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EUKaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

EUKaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

25 1 (bases 1 to 1004)

RS NIH-MGC http://mgc.nci.nih.gov.

RAL (unpublished | Martitutes of Health, Mammalian Gene Collection (MGC) (Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

found through the I.M.A.G.E. Consortium/LLNL at:

High quality Sequence start: 3

High quality Sequence start: 3

Location/Qualifiers
            121 GAGGCCGGGGCCGGGACCCTGGCCAACCCCTCGGCACCCTCAACCCGCTGAAGCTCCTG
                                                                23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    324
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                                                                                                                                                                                                                                                                                                               311 a
                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /Organism="Homo sapiens"
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/clone="#MAGE:5204452"
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Site_1: NotI; Site_2: EcoRV (destroyed); RNA source
anonymous pool of 24 week female lung, 16 week female
spleen, and 20-22 week male spleens. Library is oligo-dr
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.4 kb, insert size
rangel 1.3 kb, Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 026. Note:
a 417 c 163 g 113 t
                                                                                                                                                                                                                                    99.0%;
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                                                                                                                                  Query Match 99.0
Best Local Similarity 99.0
Matches 310; Conservative
61 TTCTTAGTGGGCTCGGCCAAGCCTGTGGCCCAGCCTGTCGCTGCGCTGGAGTCGGCGGG 120
                                                   99.0%;
                                                                                                                            Score 308.8; DB 13; Length 1059;
Pred. No. 1.3e-50;
0; Mismatches 2; Indels 0;
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Query Match	BASE COUNT	FEATURES Source	ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL COMMENT	Qy 3 Db 3: RESULT 6 BQ067622 LOCUS DEFINITION		Δb 1 Qy 1 Db 2
h 99.0%; Score 308.8; DB 13; Length 1050.	/organism="Homo sapiens" //organism="Homo sapiens" //organism="Homo sapiens" //organism="Maxon:9606" //organism="Homo:9606" //organism="DH10B" //organism="DH10B" //organism="DH10B" //organism="Denoted brain, lung, testis; vector: //orde="Organism="Denoted brain, lung, testis; vector: /	Email: cgapbs-remail.nih.gov Tissue Procurement: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLAM12793 row: m column: 17 High quality sequence stop: 343. Location/Qualifiers 11059	eleostomi; mo. n (MGC)	301 ACAGTGTTTGGC 312             323 ACAGTGTTTGGC 334  323 ACAGTGTTTGGC 334  B0067622	GAGCTGGGTCCCCAGGCCGTGGGGGCCGTGAAGGCCCTGAAGGCCCTGCTGGGGGGCCCTG	143 GAGGCCGGGGCCCTGGCCAACCCCTCGGCACCCTCAACCCGCTGAAGCTCCTG 202 181 CTGAGCAGCCTGGGCATCCCCGTGAACCACCTCATAGAGGGCTCCCAGAAGTGTGTGGCT 240

Query Match Best Local s Matches 311	BASE COUNT ORIGIN	(	FEATURES	ORGANISM REFERENCE AUTHORS TITLE JOURNAL COMMENT	LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE	Qy  Db  RESULT 7	Db Db	Qy Db	7
Natch 99.0%; score 306.8; bill; length 1007, ocal Similarity 99.4%; Pred. No. 1.3e-50; ocal Similarity 99.4%; Pred. No. 1.3e-50; ss 310; Conservative 0; Mismatches 2; Indels 0; Gaps 0; argangervative 0; Mismatches 2; Indels 0; Gaps 0; largangervative 60   Argangervative 60   Argangerva	212	/org /mola /db /clt /clt /clt /commander	Tissue cDNA I cDNA (CDNA (CDONA (CO)) (CDONA	Homo sapiens Eukaryota; M Mammalia; Eu 1 (bases 1 NIH-MGC http National Ins Unpublished Contact: Rob Email: cgapb	BM921624 1083 bp mRNA linear EST 12-MAR-2002 AGENCOURT 6707854 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5753142 5', mRNA sequence. BM921624 BM921624 GI:19372003 EST. BM921624.1 GI:19372003 EST. BM921624.1 GI:19372003	301 ACAGTGTTTGGC 312             323 ACAGTGTTGGC 334	203 CTGAGCAGCCTGGCATGCCGTGAACCCTCATAGAGGCTCCCAGAAGTGTGTGGCT 262 241 GAGCTGGGTCCCCAGGCCGTGGGGGCCCTGAAGGCCCTGAAGGCCCTGCTGGGGGCCCTG 300 241 GAGCTGGGTCCCCAGGCCGTGGGGGCCCTGAAGGCCCTGAAGGCCCTGCTGGGGGCCCTG 322 263 GAGCTGGGTCCCCAGGCCGTGGAGGCCCTGAAGGCCCTGAAGGCCCTGCTGGGGGCCCTG 322		83 THEFT ACTIGACE ANGECT GREECE AGECT GREECE
Db Qy	Query Mat Best Loca Matches Qy Db	FEATURES SOUIC BASE COUNT ORIGIN	TITLE JOURNAL COMMENT	KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS	RESULT 8 AW974727 LOCUS DEFINITION ACCESSION VERSION	Qy 2 Db 2 Qy 3 Db 3	Db 1.  Qy 1  Db 2		Db
85 TTCTTAGTGGGCTCGGCCAAGCCTGTGGCCCAGCCTGTGCGTGC	105 305 1 25	seg primer: Reverse: 1.50 1.550 2.0rganism="Homo sapiens" /mol_type="mRNA" /db_type="navan:9606" /db_xref="taxon:9606" /clone_lib="MaGE resequences, /note="Vector: pBluescriptSKm' 88 a 193 c 171 g 98 t	Assessment of gene expression patterns in a model of metastasis using a 19,200 element cDNA microarray Unpublished Contact: John Quackenbush The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 3528 Fax: 301 838 0208 Email: johngetigr.org	(human) (human) (etazoa; Chordata; Craniata; Vert theria; Primates; Catarrhini; HG to 550) (R., Abernathy, K., Dharap, S., Ga , R., Abernathy, V., Lee, N.H., Yeat J.	AW974727 EST386817 MAGE resequences, MAGN Homo sapiens cDNA, AW974727 AW974727 GI:8165915	141 GACTGGGTCCCAGGCCGTGGGGGCCGTGAAGGCCCTGAAGGCCCTGCAGGCCCTGCAGGCCCTGCAGGCCCTGCAGGCCCTGCAGGCCCTGCAGGCCCTGCAGGCCCTGCAGGCCCTGCAGGCCCTGCTGGGGGGCCCTGCTGGGGGGCCCTGCTGGGGGG	61 81 21	61 01 21	41 ATGAAGCTCGCCGCCCTCCTGGGGCTCTGCGTGGCCCTGTCCTGCAGCTCCGCTGCT

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El (Joses I to 437)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

Unpublished
Contact; Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
CDNA Library Preparation:
CDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
CDNA Library Arrayed by: The I.M.A.G.E. Consortium/LNL
Sequencing Center (NISC)
Clone distribution: NCI-CGAP clone distribution information can be info@image.llnl.gov
Plate: LLAM8008 row: J column: 10
Sear nrimer: MIRDED rowerse crimer / NEIV
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Seq primer:
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                                       GCTCGCCGCCTCCTGGGGCTCTGCGTGGCCCTGTCCTGCAGCTCCGCTCGTGCTTTCTT 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (human)
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                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                           63
                                                                                                                                                                                                                                                                   /note="Organ: prostate; vector: pT7T3D-Pac (Pharmacia)
/note="Organ: prostate; vector: pT7T3D-Pac (Pharmacia)
with a modified polylinker; plasmid DNA from the
normalized library NCI_CGAP_Pr22 was prepared, and ss
circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
this DNA was used as tracer in a subtractive hybridization
of 5,000 clones made from the same library (cloneIDs
985608-986759, 1101192-1101959, and 1217928-1220615).
Subtraction by Bento Soares and M. Fatima Bonaldo. "
a 158 c 145 g 71 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /Organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3271401"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /dev_stage="adult"
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                                                                                                                                                      0;
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Pred. No. 1.1e-49;
0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: paul mocray@ulowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Towa
cDNA Library preparation: Dr. M. Bento Soares, University
cDNA Library Arrayed by: Dr. M. Bento Soares, University of
cDNA Library Arrayed by: Dr. M. Bento Soares, University of
clone Distribution: Researchers may obtain clones from Res
Genetics (www.resgen.com) or from Open Biosystems
(www.openbiosystems.com).
Seq primer: M13 FORWARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            University of Iowa Med Labs, Iowa City, 2024 University of Iowa Med Labs, Iowa City, Tel: 319 356 4866
Fax: 319 356 7171
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1 (bases 1 to 472)

Bonaldo, M.F., Lennon, G. and Soares, M.B.
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INCF EN1-aef-n-17-0-UI.sl UI-CF-EN1 Homo sapiens UI-CF-EN1-aef-n-17-0-UI 3', mRNA sequence.
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BM977779.1 GI:19596542
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/dev_stage="Adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="U1CF_ENI"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
UI-CF-ENI is a normalized cDNA library containing the
following tissue(s): Primary Lung Cystlo Elbrosis
Epithelial Cells. The library was constructed according to
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
                                                                                                                                                                                                                                           /tissue_type="Primary Lung
Cells"
                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="rtaxon:9606"
/clone="UI-CF-EN1-aef-n-17-0-UI"
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tt90f09.x1 NCI_CGAP_Pr28
Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Emmail: cgapbs-remail.nih.gov

Emmil: cgapbs-remail.nih.gov

Emmert-Buck, M.D., Ph.D.

Emmert-Buck, M.D., Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Seq primer: -40Up from Gibco.

Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominid
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
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TAG_SEQ=CTGCTCAGGT"
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Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 961)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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National Institutes of Health, Mammalian Gene Collection, (No. 1975) (Proceedings) (Pr
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2248841"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib**NCI_CGAP_Pr28"
/clone_lib**NCI_CGAP_Pr28"
/clone_lib**NCI_CGAP_Pr28"
/clone_lib**NCI_CGAP_Pr28
/clone_lib**NCI_CGAP_Pr29
/clone_rogan: prostate; vector: plasmid DNA from the
with a modified polylinker; plasmid DNA from the
with a modified polylinker; plasmid DNA from and so
circles were made in vitro. Following HAP purification,
circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
this DNA was used as tracer in a subtractive hybridization
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/lab_host="DH10B"
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Pred. No. 1e-48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         961 bp mRNA linear EST 04-OCT-2001
Homo sapiens cDNA clone IMAGE:5174540 5',
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AUTHORS
TITLE
JOURNAL
COMMENT
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SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                     RESULT 13
BI820788
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310; Conserv
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                       Unpublished
Contact: Robert
                                                                                                 Homo sapiens (human)
Homo sapiens
Eukaryota, Metazoa; Chordata;
Mammalia; Eutheria; Primates;
1 (bases 1 to 407)
                                                                                                                                                                                                                                             BI820788 407 bp mRNA linear
603034390F1 NIH_MGC_115 Homo sapiens cDNA clone IMA
mRNA sequence.
                                                       NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, N
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//ob_xxef="taxon:9606"
//db_xxef="taxon:9606"
//clone="IMAGE:5174540"
//lab_host="DH10B"
//clone="Ibb="NIH_MGC_115"
//obe="Organ: pooled brain, lung, testis; Vector:
//note="Organ: pooled brain, lung, testis; Vector: listary is
oligo-dr primed and directionally cloned (Ecory Site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021 Note: this is a NIH_MGC Library.
03 a 308 c 277 g 172 t 1 others
t: Robert Strausberg, Ph.D
cgapbs-r@mail.nih.gov
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Pred. No. 1.7e-48;
0; Mismatches 2;
                                                                                                                      Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                            Mammalian
                                                            Gene Collection (MGC
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IMAGE:5175502 5',
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RESULT 14
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Matches 309
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cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM11437 row: c column: 23
High quality sequence start: 4
High quality sequence stop: 405.
Location/Qualifiers
                                                                                                                                                                                                                                                                                   BI490604
603032283T1 NIH_MGC_115
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 416)
                                                                                          Homo sapiens (human)
                                                                                                                                                                   EST
                                                                                                                                                                                                                                                          mRNA sequence.
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09; Conservative
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//db_xref="taxon:9606"
//db_xref="taxon:9606"
//clone="TMAGE:5175502"
//lab_host="MRNAE:5175502"
//lab_host="DHIOB"
//l
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Pred. No. 2.50
0; Mismatches
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Homo
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2;
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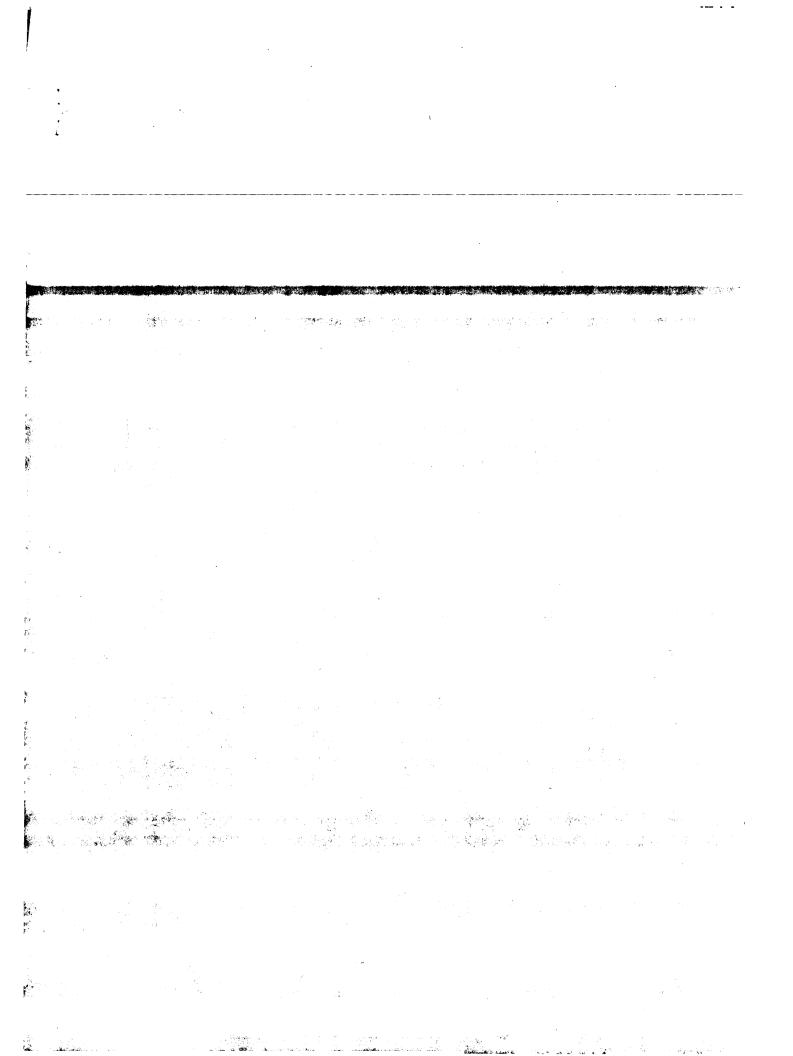
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VERSION
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BI819014
LOCUS
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214 CTGAGCAGCCTGGGCATCCCCGTGAACCACCTCATAGAGGGCTCCCAGAAGTGTGTGGCT 1.55
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Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LiAM11431 row: f column: 21
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High quality sequence stop: 416.
Location/Qualifiers
mRNA sequence.
BI819014
BI819014.1 GI:15930564
EST.
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603033130F1 NIH_MGC_115
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Pred. No. 2.5e-48;
0; Mismatches 2;
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Homo
                                                                                                                        sapiens
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REFERENCE
AUTHORS
TITLE
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11434 row: k column: 07
High quality sequence stop: 470.
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Contact: Ro
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Location/Qualifiers
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                                                              ACAGTGTTTGGC 312
|||||||||||
ACAGTGTTTGGC 332
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ilarity 99.0%;
Conservative
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cligo-dT primed and directionally cloned (EcorV site is
destroyed upon cloning). Average insert size 1.8 kb,
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Pred. No. 2.6e-48;
D; Mismatches 2
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Search completed: September 20, Job time: 1390.21 secs

2003,



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Sequence 407, Appli Sequence 4, Appli Sequence 4, Appli Sequence 47, Appli Sequence 47, Appli Sequence 13615, Appli Sequence 13615, Appli Sequence 13282, Appli Sequence 112820, Appli Sequence 71316, Appli Sequence 71316, Appli Sequence 71316, Appli Sequence 71, Appli Sequence 71, Appli Sequence 11, Appli Sequence 1219, Appli Sequence 
APPLICANT: Yumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Zhang, Zemin
ITITLE OF INVENTION: Secreted and Transmembrane Polypeptides and
ITITLE OF INVENTION: Secreted and Transmembrane Polypeptides
ITITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C13
CURRENT APPLICATION NUMBER: US/09/996,243
CURRENT FILING DATE: 2001-11-14
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-10-17
PRIOR RETLING DATE: 1997-11-12
PRIOR FILING DATE: 1997-11-12
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/06531
PRIOR FILING DATE: 1997-11-3
PRIOR FILING DATE: 1997-11-3
PRIOR FILING DATE: 1997-11-3
PRIOR FILING DATE: 1997-11-3
PRIOR FILING DATE: 1998-01-25
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PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078910
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
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US-09-996-243-407
; Sequence 407, Application US/09996243
; Sequence 407, Application US/09996243
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APPLICANT Baker, Kevin P.
APPLICANT Battein, David
APPLICANT Bestein, David
APPLICANT Eston, Dan L.
APPLICANT Ferrara, Mapoleone
APPLICANT Fong, Sherman
APPLICANT Gerber, Hanspeter
APPLICANT Geritsen, Mary E.
APPLICANT Goddward, Audrey
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APPLICANT Goddward, Applicant
APPLICANT Goddward, Applicant
APPLICANT Goddward, Audrey
APPLICANT Grinaldi, J.Christ
APPLICANT Grinaldi, J.Christ
APPLICANT Grinaldi, J.Christ
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Kljavin, Ivar J.
Napier, Mary A.
Pan, James
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Gerber, Hanspeter
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Grimaldi, J. Christopher
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US-09-41-908-1

US-09-557-440-19

US-09-52-991A-661

US-09-252-991A-6613

US-09-252-991A-6674

US-09-252-991A-6674

US-09-252-991A-6685

US-09-252-991A-6761

US-09-252-991A-7812

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Total number of hits satisfying chosen parameters:

Scoring table: Title: Perfect score: Sequence:

IDENTITY\_NUC
Gapop 10.0 , Gapext 1.0

569978 seqs, 220691566 residues

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atgaagctcgccgccctcct.....gggccctgacagtgtttggc 312

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GenCore version Copyright (c) 1993 - 2003

5.1.6 Compugen

September 19,

2003,

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i3 ; Search time 35.0684 Seconds
(without alignments)
3926.945 Million cell updates/sec

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

Result No.

Score

Match

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Description

99.0 18.1 18.1 18.1 15.8

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Issued\_Patents\_NA:\*
1: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq:\*
2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq:\*
3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq:\*
4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq:\*
5: /cgn2\_6/ptodata/2/ina/PCTUS\_COMB.seq:\*
6: /cgn2\_6/ptodata/2/ina/backfiles1.seq:\*

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US-09-522-991A-3660
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PRIOR APPLICATION NUMBER: 60/084600

PRIOR FILING DATE: 1998-05-07

PRIOR APPLICATION NUMBER: 60/087609

PRIOR PRIOR ETLING DATE: 1998-06-02

PRIOR APPLICATION NUMBER: 60/087609

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PRIOR PRIOR APPLICATION NUMBER: 60/087609

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PRIOR APPLICATION NUMBER: 60/080220

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PRIOR APPLICATION NUMBER: 60/080810

PRIOR APPLICATION NUMBER: 60/080811

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: COHEN, MAURICE
APPLICANT: FRIEDMAN, Paula N.
APPLICANT: GRODON, Julian
APPLICANT: HODGES, Steven C.
APPLICANT: KLASS, Michael R.
APPLICANT: KRASS, Michael R.
APPLICANT: ROBERTS-RAPP, Lisa
APPLICANT: ROBERTS-RAPP, Lisa
APPLICANT: STROUPE, Steven D.
APPLICANT: HOBGES:
APPLICANT: HODGES
APPLICANT: HODGE
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Patent No.
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PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09
                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                              SOFTWARE: Fastseq for Windows Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/964,725 FILING DATE:
                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
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Sequence 4, Application US/08964725

Patent NO. 5939265

Patent No. 593926

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US-08-964-725-4
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LENGTH: 263 base pairs
proper nucleic acid
                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IDM Compatible
COMPUTER: IDM Compatible
COMPUTER: DEM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FastsED for Windows Version 2.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/964,725
FILING DATE:
FILING DATE:
CLASSIFICATION NUMBER:
APPLICATION NUMBER:
APPLICATION NUMBER:
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REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 59)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
ATTORNEY AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 59
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 60064-3500
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Pred. No. 0.0026;
0; Mismatches
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                                           5997.US.P1
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0;

Gaps

256 327

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Sequence 5, Application US/08964725
PATENT NO. 5939265
GENERAL INFORMATION:
APPLICANT: COHEN, Maurice
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Best Local Similarity
Matches 93; Conserv
                                                   APPLICATION UMBER: US/08/964
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ETLING DATE:
APPLICATION NUMBER:
APPLICATION NUMBER:
APPLICATION NUMBER:
APPORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION UMBER: 35,441
REGISTRATION UMBER: 5997
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935/17/29
  TELEX:
INFORMATION FOR SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 507 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                              COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: STROUPE,
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET:
                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 60064-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE:
TELEFAX: 8
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T: HODGES, Steven C.
T: KLASS, Michael R.
T: KRATOCHVIL, Jon D.
T: ROBERTS-RAPP, Lisa
T: ROBERTS-RAPP, Lisa
T: ROSELL, John C.
T: STROUPE, Steven D.
TINVENTION: REAGENTS AND METHODS USEFUL
TINVENTION: FOR DETECTING DISEASES OF THE LUNG
TOUGHNEES: 19
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                                       847/938-2623
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ilarity 60.4%;
Conservative
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847/938†2623
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      Ö:
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                                                                                          5997.US.P1
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ITILE OF INVENTION: No. 6569662el Nucleic Acids and
ITILE OF INVENTION: Polypeptides
FILE REFERENCE: 784C1P2B
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/52,317
PRIOR APPLICATION NUMBER: 09/52,317
PRIOR TILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: pt_FIL-genes Version 1.0
LENGTH: 2497
                                                       ; OTHER INFORMATION: n = a,t,c
US-09-620-312D-47
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US-09-620-312D-47
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Best Local S
Matches 93
Query Match 15.8
Best Local Similarity 50.0
Matches 151; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Asundi, Vinod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                    NAME/KEY: misc_feature
LOCATION: (1)...(2497)
                                                                                                                                               FEATURE:
                                                                                                                                                         NAME/KEY: CDS
LOCATION: (107)..(1756)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 519 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    137 CCCTGGCCAACCCCTGGCACCCCGCTGAAGCTCCTGCTGACGACCTGGGCA 196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                197 TCCCCGTGAACCACCTCATAGAGGGCTCCCAGAAGTGTGTGGCTGAGCTGGGTCCCCAGG
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5. 6569662
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Similarity 60.4%;
93; Conservative
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Yang, Yonghong
Yang, Yonghong
Wang, Jian-Rui
Zhou, Ping
Ma, Yunging
Ma, Yunging
Wang, Dunrui
Wang, Zhiwei
John Tillinghast
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Chen, Rui-hong
Zhao, Qing A.
Wehrman, Tom
                  15.8%;
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  Score 49.2; DB 4;
Pred. No. 0.068;
0; Mismatches 148;
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RESULT 7
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US-09-252-991A-3660
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                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: MATC J. Rubenfield et al.

TITLE OF INVENTION: AUGLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AUGUSTO ACID AND THERAPEUTICS
TITLE OF INVENTION: AUGUSTO ACID AND THERAPEUTICS
TITLE OF INVENTION: AUGUSTO ACID AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 3660
LENGTH: 2274
Sequence 3615, Application US/09252991F Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3660, Application US/09252991A patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
                                                                                                                                                                                                                                                                                                                  Local Similarity
nes 109; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1099 GTACCTGGTCCCTGAGCGCGGGCCTGAGCGAGGCCTGGGCCAAGTCCCTGCGCGCCTT
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                                                                                  300 GA 301
                                                                                                                                                             208 CACCTCATAGAGGGCTCCCAGAAGTGTGTGGGTGGCTGAGGCTGGGGCCCCCAGGCCCTGGGGGCCC
                                                                                                                                                                                                                                                          112 GTCCTGGTTTCCGCCGGCAGCGCCTGCGCCCGAGTACCCGATACCCGCCAGTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63
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                                                                                                                                              TGAGCTGGGTCCCCAGGCCGTGGGGGGCCCTGAAGGCCCTGCTGGGGGGCCCT 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCTGAGCAGCCTGGGCATCCCCCGTGAACCCACCTCATAGAGGGCTCCCAGAAGTGTGTGGGC
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llarity 51.2%;
Conservative
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APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION UNMBER: US/09/252,991A
CURRENT FILING DATE: 199-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,190
PRIOR TILING DATE: 1998-07-27
NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER: DS SEQ ID NOS: 33142
SEQ ID NO 13281
LENGTH: 432
US-09-252-991A-13281
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US-09-252-991A-13281/c
US-09-252-991A-13281/c
; Sequence 13281, Application US/09252991A
; Patent No. 6551795
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-3615
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APPLICANT: MATC J. Rubenfield et al.
APPLICANT: MATC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
PRIOR FILING DATE: 1998-07-27
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SEQ ID NO 3615
LENGTH: 3297
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Best Local Similarity
Matches 109; Conserv
                                                                                                                                                                 Matches
                                                                                                                                                                                                                 Query Match
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                                                     408 CGCGGTGGGCACCGGGCTCAACGCGCCGAAGGGCTTCGCCGACGCCATCGCCGCAAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         221 TACCGGCTGCCCGAGCCGCTGGAGCAGGCGTGAACCACCTAGGCCGCCAGGCCGGC
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69 GGGCTCGGCCAAGCCTGTGGCCCAGCCTGTCGCTGCGCTGGAGTCGGCGGCGGAGGCCGG 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88 GCCCAGCCTGTCGCTGCGCTGGAGTCGGCGGGAGGCCGGGGGCCGGGACCCTGGCCAAC
                                                                                                                                                                                       Similarity
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                                                                                                           CGCCGCCCTCCTGGGGGCTCTGCGTGGCCCTGTCCTGCAGCTCCGCTCGTGCTTTCTTAGT 68
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llarity 47.2%;
Conservative
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Pred. No. 0.22;
0; Mismatches 104;
                                                                                                                                                              0;
                                                                                                                                                           Score 46.2; I
Pred. No. 0.27
0; Mismatches
                                                                                                                                                                                       DB 4;
.27;
                                                                                                                                                              158;
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                                                                                                                                                                                                                 Length 432;
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RESULT 10
US-09-252-991A-12677
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US-09-252-991A-12820
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                                   Sequence 12677, Application US/09252991A
patent No. 6551795
GENERAL INFORMATION:
APPLICANT: MATC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS A
FILE REFERENCE: 107196:136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
CURRENT FILING DATE: 1999-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: MATC J. Rubenfield et al.

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196,136

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 12820, Application US/09252991A Patent No. 6551795
GENERAL INFORMATION:
PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR FILING DATE: 1998-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Pseudomonas
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                                                                                                                 AND THERAPEUTICS
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US-09-252-91A-13122/c
US-09-252-91A
Patent No. 6551795
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: MATC J. Rubenfield et al.
APPLICANT: MATC J. Rubenfield et al.
APPLICANT: MATC J. RUCLEIC ACID AND ANINO ACID SEQUENCES RELATING TO F
TITLE OF INVENTION: NUCLEIC ACID AND ANINO ACID SEQUENCES RELATING TO F
TILE OF INVENTION UNGERS OF DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US-09/252,991A
CURRENT FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US-00/074,788
PRIOR APPLICATION NUMBER: US-00/074,788
PRIOR APPLICATION NUMBER: US-01/074,788
PRIOR APPLICATION NUMBER: US-01/074,789
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
ENOTH: 1611
TYPE: DAM
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PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 12677
LENGTH: 1428
                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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09-252-991A-13122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
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  CCTGGGCATCCCCGTGAACCACCTCATAGAGGGCTCCCAGAAGTGTGTGGCTGAGCTGGG
                                               CCACGAGCCGCTGGTCATCCTCTCCGGCGCCCTGAAGAGCCTTGGCGGTGGCCCTGATGAA
                                                                                           GGCCGGGACCCTGGCCAACCCCCTCGGCACCCTCAACCCGCTGAAGCTCCTGCTGAGCAG
                                                                                                                                          CGCCGCCGAATCGGGCCTGCCCTTCGTCGCCGCGCGCGAACAAGTTCGCCGCCCTGGCCGG
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                                                                                                                                                                                                                                                                                                                                 Score 46.2; DB Pred. No. 0.27; O; Mismatches
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TO PSEUDOMONAS

DB 4;

Length 1611;

0;

188

698

128

758 68

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721 CGCCGCCGAATCGGGCCTGCCCTTCGTCGCCGCGCGCGAACAAGTTCGCCGCCCTGGCCGG
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                                                                                                                                                                                                                         GGCCGGGACCCTGGCCACCCTCGGCACCCTCAACCCGCTGAAGCTCCTGCTGAGCAG 188
GCTGCCGGCCAACGAGCCGGGCAGCTCGATCATGCCCGGCAAGGTCAACCCGACCCAGT
                                        TCCCCAGGCCGTGGGGGCCCTGAAGGCCCTGCTGGGGGGCCCTGACAGTGT
                                                                                               GATCGCCAACGACCTGCCTGCTCGGTTCCGGCCCACGCGCCGGCTTCGCCGAGGTGAA
                                                                                                                                           CCTGGGCATCCCCGTGAACCACCTCATAGAGGGCTCCCAGAAGTGTGTGGCTGAGCTGGG 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 46.2; DB 4;
Pred. No. 0.27;
D; Mismatches 158;
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Gaps

287

110 265 170

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RESULT 13
US-09-252-91A-7185/c
Sequence 7185, Application US/09252991A
Sequence 7185, Application US/09252991A
Patent No. 6551795
Patent No. 6551795
GENERAL INFORMATION: MICHEIC ACID AND AMINO ACID SEQUENCES RELATING TO PITILE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NO.7185
SEQ ID NO.7185
LENGTH: 1083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: MAIC J: Rubenfield et al.
APPLICANT: MAIC J: Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION UMBER: US/09/252,991A

CURRENT FILING DATE: 199-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR TILING DATE: 1998-07-27

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR TILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 7316

LENGTH: 729

DRAANISM: PSEUdomonas aeruginosa

US-09-252-991A-7316
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US-09-252-991A-7316
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Best Local
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                   477
                                                                                                                                                                                                                                                                                                                                                                                                                                                         417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         131; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCGTGAAGGCCCTGAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GATCGCCAACGACCTGCGCCTGCTCGGGTTCCGGCCCACGCCGCCTTCGCCGAGGTGAA
                                                                                                                                                                                                                                                                                                                                                                                   TGGCGCTGATCCAGCAG
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pred. No. 0.67;
0; Mismatches 123;
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7304
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US-09-252-991A-7304/c
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7304, Application US/09252991A

Patent NO. 6551795

GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION UNMBER: US 60/074,788
PRIOR APPLICATION UNMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR TILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 7304

LENCTH: 1572

TYPE: DNA
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Best Local S
Matches 131
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       146 ACCCCCTCGGCACCCTCAACCCGCTGAAGCTCCTGCTGAGCAGCCTGGGCATCCCCGTGA 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              286 GGGCGCTGGCGCGCGCGCACCCAACAGTCCACGGCCGAGATCGAGACCCCTGATCGGTGCCT 227
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  CCGTGAAGGCCCTGAAG
                                                                                                                                                      ACCAGAGCGTCGACGACGCGTTGCAGACCGAGGCGGCGCTGGGCAACATCGCCACGGCGG
                                                                                           ACCACCTCATAGAGGGCTCCCAGAAGTGTGTGGCTGAGCTGGGTCCCCAGGCCGTGGGGG
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                                                                                                                                                                                                                                                                                                                                                      14.2%; Score 44.2; DB 4;
51.0%; Pred. No. 0.66;
Live 0; Mismatches 123
                        282
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Pred. No. 0.67
0; Mismatches
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TGGCGCTGATCCAGCAG

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RESULT 15
US-08-555-669-11
Sequence 11, Application US/08555669
; Sequence 17, 3248
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MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
COMPUTER: IBM PC COMPACTION
SOFTWARE: IBM PC COMPACTION
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/555,669
FILING DATE: 13 NOV-1955
FILING DATE: 13 NOV-1955
ATTORNEY/AGENT INFORMATION:
NAME: HAILUIN, ALDERT P.
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 3889-030
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-3560
TELEPHONE: 415-854-3560
TELEFAX: 415-854-3694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Qy
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; LOCATION:
US-08-555-669-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Brewton, Richard G.
APPLICANT: Mayne, Richard
TITLE OF INVENTION: TYPE IX COLLAGEN AND FRAGMENTS THEREOF
NUMBER OF SEQUENCES: | 32
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Pennie & STREET: 1155 Avenue CITY: New York STATE: New York
1391
                                                                                                                                                                                                                                                                                    1311 CGGGGTCCGGGAGGTGCCGAAGGCCCTAAGGGAGACCAGGGTATTGCAGGTTCCGACGGT 1390
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                                                                                                                                                                                                                     186 CAGCCTGGGCATCCCCGTGAACCACCTCATAGAGGGCTCCCAGAAGTGTGTGGCTGAGCT 245
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Search completed: September 20, 2003, 01:40:46
Job time: 37.0684 secs

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Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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No.
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/1/pubpna/Us07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/Us06_NEW_PUB.seq:*

3: /cgn2_6/ptodata/1/pubpna/Us06_NEW_PUB.seq:*

4: /cgn2_6/ptodata/1/pubpna/Us06_NEW_PUB.seq:*

5: /cgn2_6/ptodata/1/pubpna/Us07_NEW_PUB.seq:*

6: /cgn2_6/ptodata/1/pubpna/Us08_NEW_PUB.seq:*

7: /cgn2_6/ptodata/1/pubpna/Us08_NEW_PUB.seq:*

8: /cgn2_6/ptodata/1/pubpna/Us08_PUBCOMB.seq:*

9: /cgn2_6/ptodata/1/pubpna/Us08_PUBCOMB.seq:*

10: /cgn2_6/ptodata/1/pubpna/Us08_PUBCOMB.seq:*

11: /cgn2_6/ptodata/1/pubpna/Us09C_PUBCOMB.seq:*

12: /cgn2_6/ptodata/1/pubpna/Us09C_PUBCOMB.seq:*

13: /cgn2_6/ptodata/1/pubpna/Us09C_PUBCOMB.seq:*

14: /cgn2_6/ptodata/1/pubpna/Us10A_PUBCOMB.seq:*

15: /cgn2_6/ptodata/1/pubpna/Us10B.PUBCOMB.seq:*

16: /cgn2_6/ptodata/1/pubpna/Us10B.PUBCOMB.seq:*

16: /cgn2_6/ptodata/1/pubpna/Us10B.PUBCOMB.seq:*

17: /cgn2_6/ptodata/1/pubpna/Us06_NEW_PUB.seq:*

17: /cgn2_6/ptodata/1/pubpna/Us06_NEW_PUB.seq:*

17: /cgn2_6/ptodata/1/pubpna/Us06_NEW_PUB.seq:*
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312
1 atgaagctcgccgccctcct......gggccctgacagtgtttggc 312
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                                                                                                                                                                                                                                                                                                                    Length DB
    10
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13 US-10-081-817-3
4 US-10-227-435-6
12 US-10-227-407
12 US-10-227-407
13 US-09-989-722-407
13 US-09-989-727-407
13 US-09-989-727-407
14 US-09-989-727-407
15 US-09-989-727-407
16 US-09-991-073-407
17 US-09-991-073-407
18 US-09-991-073-407
19 US-09-991-073-407
10 US-09-991-073-407
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10 US-09-991-073-407
10 US-09-993-604-407
10 US-09-993-604-407
10 US-09-993-721-407
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Sequence 3, Appli
Sequence 6, Appli
Sequence 27, Appl
Sequence 407, App
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|-----|------------|-------------------|-------|-------|-------|-------|-------------|----------|-------|-------|-----------|-----------|----------|----------|-------|-------------------|-------|-------|-------------------|-------|-------|-------|-------|------------------|-------|-------|-------|--------|--|
| P   |            | 308.8             | 308.6 | 300.0 | 000.0 | 300.0 | 308.8       | 308.8    | 308.8 | 308.8 | 308.8     | 308.8     | 308.8    | 308.80   | 308.8 | 000.0             | 300.0 | 308.8 | 308.8             | 308.8 | 308.8 | 308.8 | 308.8 | 308.8            | 308.8 | 308.8 | 308.8 | 308.8  |  |
|     |            | 99.0              | o١    | ο١    | o١    | ρv    | oυ          | , w      | w     | Ψ     | Ψ         | w.        | Ψ,       | •        | ٠,    |                   | -     | _     | _                 |       | _     |       |       |                  |       |       |       |        |  |
|     |            | 570               | 570   | 570   | 570   | 570   | 570         | 5/0      | 570   | 570   | 570       | 570       | 570      | 570      | 570   | 570               | 770   | 570   | 570               | 570   | 570   | 570   | 570   | 570              | 570   | 570   | 570   | 570    |  |
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|     | ALIGNMENTS | US-09-997-683-407 |       | 1     | t     | ,     | ٠.          |          |       |       |           | _         | _        |          | ۲.    | US-09-990-562-407 | ۲,    | ١,    | US-09-993-00/-40/ | ċ     | 6     | -0    | 0     | -                | 0     | 0     | 0     | 0      |  |
|     |            | Sequence 407, App | 407,  | •     | 407,  | 407,  | 407,        | 407,     |       | 407   | 407,      | 40/       | 407      | 407,     | 407,  | 407,              | 407,  |       | Sequence 407, App |       | 407   | 407   | 07,   | Sequence 407 Apr | 107   | D (I  | 407   | e 407, |  |

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RESULT 2

US-10-237-435-6

Sequence 6, Application US/10237435

Publication No. US20030124580A1

GENERAL INFORMATION:
APPLICANT: WALKEY, MICHAel G.
APPLICANT: WALKEY, MICHAel G.
APPLICANT: WALKEY, Lynn E.
APPLICANT: WALKEY, Lynn E.
TITLE OF INVENTION: LUNG SURFACTANT MOLECULES
FILE REFERENCE: PB-0019 US
CURRENT APPLICATION NUMBER: US/10/237,435
CURRENT FILING DATE: 09-07-2001
PRIOR APPLICATION NUMBER: 60/317,822
PRIOR APPLICATION NUMBER: 60/317,822
PRIOR FILING DATE: 09-07-2001
SUPPRIOR FILING DATE: 09-07-2001
SUPPRIOR FILING DATE: 09-07-2001
SUPPRIOR FILING DATE: 09-07-2001
TYPE: DNA
ORGANISM: HOMO Sapiens
FEATURE:
            RESULT 3
US-10-210-951-27
Sequence 27, Application US/10210951
Publication No. US20030170228A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : NAME/KEY: misc_feature
: OTHER INFORMATION: Incyte ID No. US20030124580A1 242745.1
US-10-237-435-6
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Best Local 9
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310; Conserv
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ilarity | 99.4%;
Conservative
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NUMBER OF SEQ ID NOS: 259
SEQ ID NO 27
LENGTH: 569
TYPE: DNA
ORGANISM: Homo sapiens
US-10-210-951-27
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APPLICANT: MOCHWILLIAM I.

APPLICANT: WOOLWILLIAM I.

FILE REPERBUGE: P2931R1C1

CURRENT APPLICATION NUMBER: US/10/210,951

CURRENT APPLICATION NUMBER: US/10/210,951

CURRENT FILING DATE: 2002-08-02

PRIOR APPLICATION NUMBER: 60/014699

PRIOR APPLICATION NUMBER: 60/026943

PRIOR APPLICATION NUMBER: 60/0293

PRIOR APPLICATION NUMBER: 60/059352

PRIOR APPLICATION NUMBER: 60/059352

PRIOR RETLING DATE: 1997-07-17

PRIOR FILING DATE: 1997-00-19

PRIOR FILING DATE: 1997-10-10

PRIOR APPLICATION NUMBER: 60/062037

PRIOR APPLICATION NUMBER: 60/063045

PRIOR APPLICATION NUMBER: 60/063045

PRIOR APPLICATION NUMBER: 60/063046

PRIOR FILING DATE: 1997-10-24

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APPLICANT: Goddard, Audrey
APPLICANT: Goddwski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Marsters, Scot A.
APPLICANT: Pan James
APPLICANT: Pitti, Robert M.
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301 ACAGTGTTTGGC 312
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379 ACAGTGTTTGGC 390
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310; Conserv
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Pitti, Robert M.
Pitti, Robert Ann
Roy, Margaret Ann
Smith, Victoria
Stone, Donna M.
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Godowski, Paul J.
Gurney, Austin L.
Hillan, Kenneth J.
Marsters, Scot A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Application data removed - See File Wrapper or PALM NOS: 258
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PRIOR FILLING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088030
PRIOR APPLICATION NUMBER: 60/088033
PRIOR PILLING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088326
PRIOR APPLICATION NUMBER: 60/088326
PRIOR APPLICATION NUMBER: 60/088202
PRIOR APPLICATION NUMBER: 60/088202
PRIOR APPLICATION NUMBER: 60/088212
PRIOR APPLICATION NUMBER: 60/088212
PRIOR APPLICATION NUMBER: 60/088217
PRIOR PILLING DATE: 1998-06-05
PRIOR PILLING DATE: 1998-06-05
PRIOR PILLING DATE: 1998-06-10
PRIOR PRIOR PILLING DATE: 1998-06-10
PRIOR PILLING DATE: 1998-06-10
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PRIOR PILLING DATE: 1998-06-10
PRIOR PRILING DATE: 1998-06-10
PRIOR PPLICATION NUMBER: 60/08826
PRIOR PILLING DATE: 1998-06-10
PRIOR PPLICATION NUMBER: 60/088861
PRIOR PPLICATION NUMBER: 60/089514
PRIOR PPLICATION NUMBER: 60/089512
PRIOR PPLICATION NUMBER: 60/089514
PRIOR PPLICATION NUMBER: 60/089515
PRIOR PRIOR PPLICATION NUMBER: 60/089517
PRIOR PRILING DATE: 1998-06-16
PRIOR PPLICATION NUMBER: 60/089519
PRIOR PPLICATION NUMBER: 60/08953
PRIOR PPLICATION NUMBER: 60/08953
PRIOR PPLICATION NUMBER: 60/08953
PRIOR PPLICATION NUMBER: 60/08959
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PRIOR FILING DATE: 1998-06-24
PRIOR PRILICATION NUMBER: 60/090431
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090435
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090444
PRIOR APPLICATION NUMBER: 60/090444
PRIOR APPLICATION NUMBER: 60/090445
PRIOR APPLICATION NUMBER: 60/090445
PRIOR APPLICATION NUMBER: 60/090472
PRIOR APPLICATION NUMBER: 60/090535
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090535
PRIOR APPLICATION NUMBER: 60/090540
PRIOR FILING DATE: 1998-06-24
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Matches 310
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OR APPLICATION NUMBER: 60/090694
OR FILING DATE: 1998-06-25
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OR FILING DATE: 1998-06-25
OR FILING DATE: 1998-06-25
OR APPLICATION NUMBER: 60/090862
OR FILING DATE: 1998-06-26
OR APPLICATION NUMBER: 60/090863
OR FILING DATE: 1998-06-26
OR APPLICATION NUMBER: 60/091360
OR FILING DATE: 1998-07-01
OR APPLICATION NUMBER: 60/091360
OR FILING DATE: 1998-07-02
OR APPLICATION NUMBER: 60/091544
OR APPLICATION NUMBER: 60/091544
OR APPLICATION NUMBER: 60/091544
OR APPLICATION NUMBER: 60/091544
OR APPLICATION NUMBER: 60/09154
OR APPLICATION NUMBER: 60/09152
OR APPLICATION NUMBER: 60/09152
                                                                                                                                                                                                                                                                                                                 OR APPLICATION NUMBER: 60/091633
OR FILING DATE: 1998-07-02
OR PAPPLICATION UNMBER: 60/091978
OR APPLICATION NUMBER: 60/091982
OR FILING DATE: 1998-07-07
OR APPLICATION NUMBER: 60/092182
OR APPLICATION NUMBER: 60/092182
OR FILING DATE: 1998-07-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R APPLICATION NUMBER: 60/09
R FILING DATE: 1998-06-24
R APPLICATION NUMBER: 60/09
R APPLICATION NUMBER: 60/09
R FILING DATE: 1998-06-25
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FILING DATE: 1998-06-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                           121
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310; Conserv
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ilarity |99.4%;
Conservative
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Patent No.
GENERAL IN
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APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Botstein, David
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Ferrara, Napoleone
APPLICANT: Gereitsen, Mary E.
APPLICANT: Gereitsen, Mary E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            199 GAGGCCGGGGCCGGGACCCTGGCCAACCCCTCGGCACCCTCAACCCGCTGAAGCTCCTG
                                                                                                                                                                                                                                                           US20020072092A1
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ACAGTGTTTGGC 390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Desnoyers, Luc
Eaton, Dan L
Ferrara, Napoleone
                                                                                                                                                                                                                                                                                  Application US/09989723
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|              |              |            |              |                |                  |              |             |              |            |                  |              |             |              |            |              |         |            |            |             | _           |             |             |             |             |             |             | _           |             |             |             |             |             |             |             |             |             |             |             |             | _           |             |             |             |             |             |            |         |            |                   |             |                    |             |         |       |            |             |         |         |            |         |            |                |           |         |            |             | _     |
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|              | PRIOR        | PRIOR      | PRIOR        | TRIOR<br>TOTAL | מאדטוג אינו      | 77.107       | מאוכא       | מאלוטגיים ו  | 177.07     | 20102            | STOR         | PRIOR       | PRIOR        | PRIOR      | PRIOR        | PRIOR   | PRIOR      | PRIOR      | PRIOR       | PRIOR       | PRIOR       | PRIOR       | PRIOR       | PRIOR       | PRIOR       | PRIOR       | PRIOR       | PRIOR       | PRIOR       | PRIOR       | PRIOR       | PRIOR       | PRIOR       | PRIOR       | PRIOR       | PRIOR       | PRIOR       | PRIOR       | ROTOR       | PRIOR       | מאבוטאי     | TRIOR       | PRIOR       | PRIOR       |             |            |         |            | PRIOR             |             |                    | IOR         | $\pi$   |       | ק ס        | N C C       | 2       | , 20    | PRIOR      | 20      | RIOR       | DRIOR<br>ROLUK | RIOR      | RIOR    | RIOR       | PRIOR       | aCT a |
| 4 + Ch       | DAT          | CATIO      | H #          | TAL            | 1 K              | DITION       | TEND THE    | TLING        | ) H        | NOT TO THE       | JAC.         | APPLICATION | ILING DAT    | IC         | ILING DAT    | PPLICE  | ILIN       | Ĕ          | FILING DATE | APPLICATION | APPLICATION | FILING DATE | APPLICATION | FILING DATE | APPLICATION | DATE       | ATION   | DATE       | ATION             | 7 1 1 1 1 1 | DATE               | APPLICATION | DATE    | S i   |            | 7 7         | PILE    | DATE    | ž          | DATE    | LICATION   | STITUG DATE:   | NG DAT    | ICATION | DAT        | APPLICATION | DATE  |
| 99 08. SCOTE | : 1998-07-09 | NUMBER: 60 | : 1998-07-07 | NIIMBER.       | NUMBER: 60/0919/ | . 1990 07 02 | . 1999-07-0 | : 1996-0/-02 | 1008-07-03 | NITMBER: 60/0916 | . 1998-07-02 | NUMBER: 6   | : 1998-07-01 | NUMBER: 60 | : 1998-07-02 | NUMBER: | 1998-07-01 | NUMBER: 60 | 198-00-56   | NUMBER: 60  | 1998-06-26  | NUMBER: 60  | 1998-06-25  | NUMBER: 60  | 1998-06-24  | NUMBER: 60  | 1998-06-24  | NUMBER:     | 1998-06-24  | NUMBER:     | NOMBER:     | 1998-00-24  | NOMBER:     | 1998-06-24  | NUMBER:     | 1998-06-24 | NUMBER: | 1998-06-24 | NUMBER: 60/090435 | 1998-06-24  | 5-U5-24<br>5-U5-24 | ) E         | 8-06-23 | ER: 6 | 1998-06-23 | 50 · 00 · 2 | MUEK: 0 | 8-06-22 | NUMBER: 60 | 8-06-22 | NUMBER: 60 | 1998-06-19     | T-90-866T | NUMBER: | 1998-06-19 | NUMBER: 60  | 1998- |
| 308 8.       |              |            |              |                |                  |              |             |              |            |                  |              |             |              |            |              |         |            |            |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |            |         |            |                   |             |                    |             |         |       |            |             |         |         |            |         |            |                |           |         |            |             |       |
| DB 9:        |              |            |              |                |                  |              |             |              |            |                  |              |             |              |            |              |         |            |            |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |            |         |            |                   |             |                    |             |         |       |            |             |         |         |            |         |            |                |           |         |            |             |       |
| I.engt       |              |            |              |                |                  |              |             |              |            |                  |              |             |              |            |              |         |            |            |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |            |         |            |                   |             |                    |             |         |       |            |             |         |         |            |         |            |                |           |         |            |             |       |

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PRIOR FILLING DATE: 1998-06-03
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PRIOR APPLICATION NUMBER: 60/088026
PRIOR FILLING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088026
PRIOR PRILING DATE: 1998-06-04
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PRIOR APPLICATION NUMBER: 60/088029
PRIOR APPLICATION NUMBER: 60/088033
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PRIOR APPLICATION NUMBER: 60/088033
PRIOR PILLING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088033
PRIOR APPLICATION NUMBER: 60/088033
PRIOR PILLING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088033
PRIOR PRILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088212
PRIOR APPLICATION NUMBER: 60/089212
PRIOR APPLICATION NUMBER: 60/08921

Query Match 99.0%; Score 308.8; DB 9; Length 570;

| ELLE REFERENCE: 92/30P1C36  CURRENT APPLICATION NUMBER: US/09/989,279  CURRENT FILING DATE: 2001-11-19  PRIOR APPLICATION NUMBER: 60/049787  PRIOR FILING DATE: 1997-66-16  PRIOR FILING DATE: 1997-66-16  PRIOR PRIOR APPLICATION NUMBER: 60/62250  PRIOR APPLICATION NUMBER: 60/65286  PRIOR APPLICATION NUMBER: 60/65316  PRIOR PRIOR DATE: 1997-11-13  PRIOR APPLICATION NUMBER: 60/66531  PRIOR APPLICATION NUMBER: 60/66770  PRIOR APPLICATION NUMBER: 60/075945  PRIOR PILING DATE: 1997-11-24  PRIOR APPLICATION NUMBER: 60/075945 | GENERAL INFORMATION:  APPLICANT: AShkenazi.Avi J.  APPLICANT: Baker.Kevin P.  APPLICANT: Betstein, David  APPLICANT: Betstein, David  APPLICANT: Eaton, Dan I.  APPLICANT: Ferrara, Napoleone  APPLICANT: Ferrara, Napoleone  APPLICANT: Ferrara, Napoleone  APPLICANT: Gerber, Hanspeter  APPLICANT: Gerier, Hanspeter  APPLICANT: Godowski.Paul J.  APPLICANT: Godowski.Paul J.  APPLICANT: Grimaldi.J.Christopher  APPLICANT: Grimaldi.J.Christopher  APPLICANT: Napier, Mary. A.  APPLICANT: Napier, Mary.  APPLICANT: Napier Asy.  APPLICANT: Paoni, Nicholas F.  APPLICANT: Paoni, Nicholas F.  APPLICANT: Stewart, Timothy A.  APPLICANT: Stewart, Timothy A.  APPLICANT: Watinabe, Colin K.  APPLICANT: Watinabe, Colin K.  APPLICANT: Watinabe, Colin K.  APPLICANT: Watinabe, Zemin  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic | Hest Local Similarity   99.4%; Pred. No. 1e-63;  Watches 310; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  Y 1 ATGAAGCTGGCCGCCCTCCTGGGGCTTGCGTGGCCTGCAGCTCCGCTGGTGCT 60                                                                                                                                                                                                              |
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PRIOR APPLICATION NUMBER: 60/089599
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089600
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PRIOR PILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089801
PRIOR APPLICATION NUMBER: 60/089801
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PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089907
PRIOR PILING DATE: 1998-06-18

APPLICATION NUMBER: 60/089598 FILING DATE: 1998-06-17

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RESULT 7
US-09-989-727-407
; Sequence 407, Ap
; Patent No. US200
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PRIOR APPLICATION NUMBER: 60/091626
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PRIOR EILING DATE: 1998-07-02
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Best Local S
Matches 310
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APPLICANT:
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APPLICANT:
APPLICANT:
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C65
                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 TTCTTAGTGGGCTCGGCCAAGCCTGTGGCCCAGCCTGTCGCTGCGCTGGAGTCGGCGGCG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION:
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Similarity 99.4%;
10; Conservative
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US20020072497A1
                                                                                                                                                                               Eaton, Dan L.
Eaton, Dan L.
Ferrara Napoleone
Fong, Sherman
Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Kijavin, Ivar J.
                                                                                                                                                                                                                                                                                                                                                    Ashkenazi, Avi J.
Raker, Kevin P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACAGTGTTTGGC 312
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                                                                                                                                                                                                                                                                                                                        Baker, Kevin P.
Botstein, David
Desnoyers, Luc
                                                    Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
Zhang "omin
                                                                                                   Roy, Margaret Ann
Stewart, Timothy
Tumas, Daniel
                                                                                                                                           Paoni,
                                                                                                                                                       Napier, Mary A.
Pan, James
                                                                                                                                           Nicholas F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 308.8; DB 9;
Pred. No. 1e-63;
0; Mismatches 2;
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PRIOR FILLING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089908
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PRIOR APPLICATION NUMBER: 60/089947
PRIOR APPLICATION NUMBER: 60/089948
PRIOR APPLICATION NUMBER: 60/09952
PRIOR APPLICATION NUMBER: 60/090254
PRIOR PRILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/090254
PRIOR APPLICATION NUMBER: 60/090254
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PRIOR APPLICATION NUMBER: 60/090359
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PRIOR PILLING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090449
PRIOR PILLING DATE: 1998-06-24
PRIOR PILLING DATE: 1998-06-24
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PRIOR APPLICATION NUMBER: 60/090444
PRIOR APPLICATION NUMBER: 60/090444
PRIOR APPLICATION NUMBER: 60/090445
PRIOR APPLICATION NUMBER: 60/090447
PRIOR APPLICATION NUMBER: 60/090447
PRIOR APPLICATION NUMBER: 60/090540
PRIOR APPLICATION NUMBER: 60/090557
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| PRIOR PILLING DATE: 1998-06-11 PRIOR PILLING DATE: 1998-06-12 PRIOR PILLING DATE: 1998-06-16 PRIOR PILLING DATE: 1998-06-16 PRIOR APPLICATION UNMBER: 60/089512 PRIOR PILLING DATE: 1998-06-16 PRIOR PILLING DATE: 1998-06-16 PRIOR PILLING DATE: 1998-06-16 PRIOR PILLING DATE: 1998-06-16 PRIOR PILLING DATE: 1998-06-17 PRIOR PILLING DATE: 1998-06-18 PRIOR PILLING DATE: 1998-06-19 PRIOR PILLING DATE: 1998-06-19 PRIOR PILLING DATE: 1998-06-19 PRIOR PILLING DATE: 1998-06-19 PRIOR PILLING DATE: 1998-06-20 PRIOR PILLING DATE: 1998-06-22 PRIOR PILLING DATE: 1998-06-22 PRIOR PILLING DATE: 1998-06-23 PRIOR APPLICATION NUMBER: 60/090254 PRIOR PILLING DATE: 1998-06-23 PRIOR PILLING DATE: 1998-06-24 PRIOR APPLICATION NUMBER: 60/09044 PRIOR PRILING DATE: 1998-06-24 PRIOR PRILING DATE: 1998-06-25 PRIOR PRILING DATE: 1998-06-25 P |                                                    |                                                    |                                    |                              |            |                                |                  |                  |                                |            |            |                                |                  |                  |                  |            |            |            |                  |                  |            |            |                                |                  | •                |                                |              | -            |                  |                 |                                | _          |              | -                |                  |              |              |              |                  |                  |
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| PRIOR FILING DATE: 1998-06-11 PRIOR APPLICATION NUMBER: 60/08910 PRIOR FILING DATE: 1998-06-12 PRIOR APPLICATION NUMBER: 60/08951 PRIOR FILING DATE: 1998-06-16 PRIOR FILING DATE: 1998-06-16 PRIOR FILING DATE: 1998-06-17 PRIOR FILING DATE: 1998-06-17 PRIOR FILING DATE: 1998-06-17 PRIOR PPLICATION NUMBER: 60/08953 PRIOR FILING DATE: 1998-06-17 PRIOR APPLICATION NUMBER: 60/08959 PRIOR FILING DATE: 1998-06-17 PRIOR APPLICATION NUMBER: 60/08959 PRIOR FILING DATE: 1998-06-17 PRIOR APPLICATION NUMBER: 60/08959 PRIOR FILING DATE: 1998-06-17 PRIOR APPLICATION NUMBER: 60/08960 PRIOR FILING DATE: 1998-06-17 PRIOR APPLICATION NUMBER: 60/08990 PRIOR FILING DATE: 1998-06-17 PRIOR APPLICATION NUMBER: 60/08990 PRIOR FILING DATE: 1998-06-18 PRIOR PRIOR PRICATION NUMBER: 60/08990 PRIOR FILING DATE: 1998-06-18 PRIOR APPLICATION NUMBER: 60/08990 PRIOR FILING DATE: 1998-06-18 PRIOR APPLICATION NUMBER: 60/08994 PRIOR APPLICATION NUMBER: 60/09094 PRIOR APPLICATION NUMBER: 60/09094 PRIOR APPLICATION NUMBER: 60/09024 PRIOR APPLICATION NUMBER: 60/09025 PRIOR FILING DATE: 1998-06-23 PRIOR PRILING DATE: 1998-06-23 PRIOR PRILING DATE: 1998-06-23 PRIOR PRILING DATE: 1998-06-24 PRIOR APPLICATION NUMBER: 60/09041 PRIOR APPLICATION NUMBER: 60/09041 PRIOR APPLICATION NUMBER: 60/09041 PRIOR PRILING DATE: 1998-06-24 PRIOR APPLICATION NUMBER: 60/09041 PRIOR APPLICATION NUMBER: 60/09041 PRIOR PRILING DATE: 1998-06-24 PRIOR PRILING DATE: 1998-06-25 PRIOR FILING DATE: 1998-06-25 PRIOR PRILING DATE: 1998-06-25 PRIOR PRILING DATE: 1998-06-25 PRIOR PRILING DATE: 1998-06-25 PRIOR PRIOR PRICATION NU | ****                                               |                                                    |                                    |                              |            | ٠, ٠,                          | ٠. ٠             |                  | ·· ··                          | ٠. ٠       |            | ٠. ٠.                          | ٠. ٠             | ٠                | ٠. ٠.            |            |            | ·• •·      | ٠                |                  | ·· ·       |            |                                |                  |                  | ·. ·.                          | ••           |              | ٠. ،             |                 | ·. ·.                          | ٠          |              |                  |                  | •• ••        |              |              | ٠                |                  |
| APPLICATION NUMBER: 60/09944 FILING DATE: 1998-06-11 APPLICATION NUMBER: 60/08944 FILING DATE: 1998-06-16 APPLICATION NUMBER: 60/08944 FILING DATE: 1998-06-16 APPLICATION NUMBER: 60/08951 FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/08953 APPLICATION NUMBER: 60/08953 APPLICATION NUMBER: 60/08953 APPLICATION NUMBER: 60/08959 FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/08959 FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/08960 APPLICATION NUMBER: 60/08960 APPLICATION NUMBER: 60/08960 FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/08960 FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/08980 APPLICATION NUMBER: 60/08990 FILING DATE: 1998-06-18 APPLICATION NUMBER: 60/08990 FILING DATE: 1998-06-18 APPLICATION NUMBER: 60/08990 FILING DATE: 1998-06-19 APPLICATION NUMBER: 60/08991 FILING DATE: 1998-06-19 APPLICATION NUMBER: 60/09094 APPLICATION NUMBER: 60/09095 APPLICATION NUMBER: 60/09095 APPLICATION NUMBER: 60/09044 FILING DATE: 1998-06-23 APPLICATION NUMBER: 60/09044 FILING DATE: 1998-06-23 APPLICATION NUMBER: 60/09044 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/09044 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/09044 APPLICATION NUMBER: 60/09055 APPLICATION NUMBER: 60/09056 APPLICATI | RIOR<br>RIOR<br>RIOR                               | RIOR                                               | RIOR                               | RIOR                         | RIOR       | RIOR                           | RIOR             | RIOR             | RIOR                           | RIOR       | RIOR       | RIOR                           | RIOR             | IOR              | IOR              | IOR        | RIOR       | RIOR       | RIOR             | PRIOR            | PRIOR      | PRIOR      | PRIOR                          | PRIOR            |                  | RI                             | H            | нн           | Hi               |                 | 진진                             | 2 2        | RIO          | RIO              | RIC              | RIO          | RIO          | RIO          | RIO              | RIO              |
| NUMBER: 60/08951 NUMBER: 60/08951 1998-06-16 NUMBER: 60/08951 1998-06-16 NUMBER: 60/08951 1998-06-17 NUMBER: 60/08953 NUMBER: 60/08953 NUMBER: 60/08959 1998-06-17 NUMBER: 60/08959 1998-06-17 NUMBER: 60/08960 1998-06-18 NUMBER: 60/08980 1998-06-18 NUMBER: 60/08990 1998-06-18 NUMBER: 60/08990 1998-06-18 NUMBER: 60/08991 1998-06-18 NUMBER: 60/08994 1998-06-29 NUMBER: 60/08994 1998-06-29 NUMBER: 60/09024 1998-06-27 NUMBER: 60/09044 1998-06-28 NUMBER: 60/09044 1998-06-24 NUMBER: 60/09044 1998-06-25 NUMBER: 60/090559 1998-06-25 NUMBER: 60/090540 1998-06-25 NUMBER: 60/090540                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | PPLICATION TLING DATE: PPLICATION TLING DATE:      | PPLICATION TILING DATE: PPLICATION TLING DATE:     | TILING DATE:                       | PPLICATION                   | TLING DATE | PPLICATION                     | PPLICATION       | PPLICATION       | PPLICA                         | TLING      | ILING DATE | PPLICATION                     | PPLICATION       | PPLICATION       | PPLICATION       | ILING DATE | TLING DATE | ILING DATE | PPLICATION       | PPLICATION       | ILING DATE | ILING DATE | PELICATION                     | PPLICATION       | PPLICATION       | PPLICATION                     | ILING E      | ILING I      | PPLICA           | PPLICA          | PPLICA                         | ILING      | ILING DA     | PPLICATI         | PPLICATI         | LING DAT     | ILING DAT    | PPLICATIO    | CATIO            | PLICATIO         |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | ER: 60/09069<br>8-06-25<br>ER: 60/09069<br>8-06-25 | ER: 60/09067<br>8-06-25<br>ER: 60/09069<br>8-06-25 | 8-06-24<br>ER: 60/09067<br>8-06-25 | ER: 60/09055<br>ER: 60/09055 | 1998-06-24 | 1998-06-24<br>NUMBER: 60/09054 | NUMBER: 60/09053 | NUMBER: 60/09047 | NUMBER: 60/09044<br>1998-06-24 | 1998-06-24 | 1998-06-24 | 1998-06-24<br>NUMBER: 60/09043 | NUMBER: 60/09043 | NUMBER: 60/09042 | NUMBER: 60/09035 | 1998-06-23 | 1998-06-22 | 1998-06-22 | NUMBER: 60/09025 | NUMBER: 60/09024 | 1998-06-19 | 1998-06-19 | 1998-06-19<br>NUMBER: 60/08994 | NUMBER: 60/08994 | NUMBER: 60/08990 | NUMBER: 60/08990<br>1998-06-18 | : 1998-06-18 | : 1998-06-17 | NUMBER: 60/08965 | NUMBER: 60/0896 | NUMBER: 60/08959<br>1998-06-17 | 1998-06-17 | : 1998-06-17 | NUMBER: 60/08953 | NUMBER: 60/08953 | : 1998-06-16 | : 1998-06-16 | : 1998-06-16 | NUMBER: 60/08944 | NUMBER: 60/08910 |

CUURRENT APPLICATION NUMBER: US/09/989,727
CUURRENT ETLING DATE: 12001-11-19
PRIOR FILLING DATE: 1207-06-16
PRIOR FILLING DATE: 1997-06-16
PRIOR FILLING DATE: 1997-11-12
PRIOR PAPLICATION UNMBER: 60/065311
PRIOR PAPLICATION UNMBER: 60/065311
PRIOR PAPLICATION UNMBER: 60/075945
PRIOR PAPLICATION UNMBER: 60/075945
PRIOR PELLING DATE: 1998-02-25
PRIOR PELLING DATE: 1998-03-20
PRIOR PELLING DATE: 1998-05-07
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PRIOR PELLING DATE: 1998-06-04
PRIOR PELLING DATE: 1998-06-05
PRIOR PELLING DATE: 1998-06-10
PRIOR PELLING DATE: 1998-06

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RESULT 8
US-09-989-731-407
Sequence 407, Ap
                       Sequence 407, Application US/09989731
Patent No. US/20020103125A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Bensoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Ferrara, Napoleone
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Paull J.
APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Austin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OR APPLICATION NUMBER: 60/090696
OR FILING DATE: 1998-06-25
OR APPLICATION NUMBER: 60/090862
OR APPLICATION NUMBER: 60/090863
OR FILING DATE: 1998-06-26
OR APPLICATION NUMBER: 60/091360
OR APPLICATION NUMBER: 60/091478
OR APPLICATION NUMBER: 60/091544
OR APPLICATION NUMBER: 60/091544
OR FILING DATE: 1998-07-01
OR APPLICATION NUMBER: 60/091519
OR APPLICATION NUMBER: 60/091519
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Fong, Sherman
Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J.Christopher
Gurney, Austin L.
Kljavin, Ivar J.
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CURRENT APPLICATION NUMBER: US/09/989/731
CURRENT EILING DATE: 2001-11-20
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PRIOR APPLICATION NUMBER: 60/062250
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PRIOR APPLICATION NUMBER: 60/065311
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PRIOR PPLICATION NUMBER: 60/075945
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PRIOR APPLICATION NUMBER: 60/075945
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PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/08322
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C70
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Stewart, Timothy A.
Tumas, Daniel
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Pan, James
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Matches Query Match Best Local :

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RESULT 9
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J. Sequence 407, Application US/09989732
Ratent NO. US20020133463A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
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OR APPLICATION NUMBER: 60/091519
OR APPLICATION NUMBER: 60/09154
OR APPLICATION NUMBER: 60/09154
OR APPLICATION NUMBER: 60/09159
OR FILING DATE: 1998-07-02
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OR FILING DATE: 1998-07-02
OR APPLICATION NUMBER: 60/09163
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al Similarity 99.4%;
310; Conservative
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                                                                                                                                                                                                                                                                                                                                                       312
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Pred. No. 1e-63;
0; Mismatches 2;
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OR APPLICATION NUMBER: 60/088742
OR FILING DATE: 1998-06-10
OR APPLICATION NUMBER: 60/088810
OR APPLICATION NUMBER: 60/088826
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| PRIOR FILING DATE: 1998-06-10 PRIOR APPLICATION NUMBER: 60/08824 PRIOR APPLICATION NUMBER: 60/088824 PRIOR FILING DATE: 1998-06-10 PRIOR APPLICATION NUMBER: 60/088826 PRIOR FILING DATE: 1998-06-11 PRIOR APPLICATION NUMBER: 60/088861 PRIOR FILING DATE: 1998-06-11 PRIOR APPLICATION NUMBER: 60/088861 PRIOR APPLICATION NUMBER: 60/089105 PRIOR APPLICATION NUMBER: 60/089105 PRIOR FILING DATE: 1998-06-16 PRIOR FILING DATE: 1998-06-16 PRIOR FILING DATE: 1998-06-16 PRIOR FILING DATE: 1998-06-16 PRIOR APPLICATION NUMBER: 60/089514 PRIOR APPLICATION NUMBER: 60/089514 PRIOR APPLICATION NUMBER: 60/089538 PRIOR APPLICATION NUMBER: 60/089538 PRIOR APPLICATION NUMBER: 60/089538 PRIOR APPLICATION NUMBER: 60/089538 PRIOR APPLICATION NUMBER: 60/089599 PRIOR FILING DATE: 1998-06-17 PRIOR PILING DATE: 1998-06-17 PRIOR PILING DATE: 1998-06-17 PRIOR PILING DATE: 1998-06-17 PRIOR PILING DATE: 1998-06-17 PRIOR APPLICATION NUMBER: 60/089599 PRIOR APPLICATION NUMBER: 60/089599 PRIOR FILING DATE: 1998-06-18 PRIOR APPLICATION NUMBER: 60/08960 PRIOR APPLICATION NUMBER: 60/08960 PRIOR APPLICATION NUMBER: 60/089908 PRIOR APPLICATION NUMBER: 60/089908 PRIOR APPLICATION NUMBER: 60/089908 PRIOR APPLICATION NUMBER: 60/089908 PRIOR PILING DATE: 1998-06-18 PRIOR APPLICATION NUMBER: 60/089908 PRIOR APPLICATION NUMBER: 60/089908 PRIOR APPLICATION NUMBER: 60/089908 PRIOR APPLICATION NUMBER: 60/089908 PRIOR APPLICATION NUMBER: 60/089940 PRIOR APPLICATION NUMBER: 60/089940 PRIOR PILING DATE: 1998-06-19 PRIOR APPLICATION NUMBER: 60/089940 PRIOR APPLICATION NUMBER: 60/089940 PRIOR APPLICATION NUMBER: 60/089940 PRIOR FILING DATE: 1998-06-19 PRIOR APPLICATION NUMBER: 60/089940 PRIOR APPLICATION NUMBER: 6 | FILING DATE: APPLICATION N |

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Matches 310
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APPLICANT: ABNORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Baker, Kevin P.
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APPLICANT: Besnoyers, Luc
APPLICANT: Escanoyers, Luc
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APPLICANT: Gerristsenkery E.
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; Sequence 407, Application US/09991073
; Patent No. US20020127576A1
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PRIOR APPLICATION NUMBER: 60/088217
PRIOR APPLICATION NUMBER: 60/088734
PRIOR FILING DATE: 1998-06-09
PRIOR APPLICATION NUMBER: 60/088742
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APPLICANT: Ashkenzi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Baker, Kevin P.
APPLICANT: Beststein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Desnoyers, Luc
APPLICANT: Desnoyers, Luc
APPLICANT: Eston, David
APPLICANT: Ferrara, Napoleone
APPLICANT: Ferrara, Napoleone
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Gerber, Hanspeter
APPLICANT: Godowski, Paul J
APPLICANT: Godowski, Paul J
APPLICANT: Godowski, Paul J
APPLICANT: Godowski, Paul J
APPLICANT: Kljavin, Ivar J.
APPLICANT: Roy, Margaret Ann
APPLICANT: Roy, Margaret Ann
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT
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PRIOR APPLICATION NUMBER: 60/090696
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PRIOR PILING DATE: 1998-02-25
PRIOR PEPLICATION NUMBER: 60/075945
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PRIOR PELING DATE: 1998-04-28
PRIOR PELING DATE: 1998-05-07
PRIOR PELING DATE: 1998-06-02
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PRIOR PELING DATE: 1998-06-04
PRIOR PELICATION NUMBER: 60/088029
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Matches 310; Conservative
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Fong, Sherman
Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
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Baker, Kevin P.
Botstein, David
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
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Eaton, Dan L.
                                                                                               Napier, Mary A.
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; Sequence 407, Application US/09990456
; Patent NO. US20020137890A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Gerber,Honspeter
; APPLICANT: Gerritsen,Mary E.
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PRIOR APPLICATION NUMBER: 60/089512
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APPLICANT: TURNER, Daniel
APPLICANT: Wattanabe, Colin K.
APPLICANT: Wattanabe, Colin K.
APPLICANT: Wattanabe, Colin K.
APPLICANT: Whilliam I.
APPLICANT: Whod, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Replicant Replication Number: 50/08/989,721
CURRENT FILING DATE: 1937-06-16
PRIOR APPLICATION UNMER: 60/08/977
PRIOR APPLICATION UNMER: 60/08/977
PRIOR PRILING DATE: 1997-06-16
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Patent No. US20020142961A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, And J.
APPLICANT: Botstein, David
APPLICANT: Botstein, David
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-989-721-407
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o. US20020142961A1
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Goddard, Audrey
Godowski, Paul J
Grimaldi, J. Christopher
Gurney, Austin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gerber, Hanspeter
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art, Timothy A.
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Query Match Best Local Matches

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RESULT 15

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OR FILING DATE: 1998-06-04
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OR FILING DATE: 1998-06-10
OR APPLICATION NUMBER: 60/088738

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OR APPLICATION NUMBER: 60/09163
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OR APPLICATION NUMBER: 60/09157
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                                    GAGGCCGGGGCCGGGACCCTGGCCAACCCCTCGGCACCCTCAACCCGCTGAAGCTCCTG
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Pred. No. 1e-63;
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OR FILING DATE: 1998-06-22
OR FILING DATE: 1998-06-23
OR FILING DATE: 1998-06-22
OR APPLICATION NUMBER: 60/090255
OR FILING DATE: 1998-06-23

| Search<br>Job tim                                      | Db 43        | Ov Db                                                  | D Qy                                                                 | Db          |
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| Search completed: September<br>Job time : 128.366 secs | ACAGTGTTTGGC | GAGCTGGGTC                                             | GAGCTGGGTC                                                           | CTGAGCAGCC  |
| per 20, 2003, 03:21:36                                 |              | CCA6GCCGTGGGGGCCGTGAAGGCCCTGAAGGCCCTGCTGGGGGGCCCTG 378 | GAGCTGGGTCCCCAGGCCGTGGGGGGCCCTGAAAGGCCCTGAAAGGCCCTGCTGGGGGGCCCTG 300 |             |
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Title:
Perfect score:
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Maximum Match 100%
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Maximum DB
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Copyright (c) 1993 - 2003
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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| 312 100.0<br>312 100.0<br>312 100.0<br>312 100.0<br>308.8 99.0                   | Query<br>Match           |
| 312<br>312<br>461<br>446                                                         | Query<br>Match Length DB |
| 1<br>45<br>53<br>21                                                              | . ₩                      |
| PCT-US02-05403-3 5 US-10-081-817-3 GS-10-631-467-467 US-09-489-036-35171         | Length DB ID             |
| Sequence 3, Appli<br>Sequence 3, Appli<br>Sequence 467, App<br>Sequence 35171, A | Description              |

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RESULT 1

PCT-US02-05403-3

Sequence 3, Application PC/TUS0205403

Sequence 3, Application PC/TUS0205403

GENERAL INFORMATION:

APPLICANT: Dana-Farber Cancer Institute, Inc.

TITLE OF INVENTION. HIN-1, A TUMOR SUPPRESSOR GENE

FILE REFERENCE: 00530-094WO1

CURRENT APPLICATION NUMBER: PCT/US02/05403

CURRENT FILING DATE: 2002-02-22

PRIOR APPLICATION NUMBER: 60/270,973

PRIOR APPLICATION NUMBER: 60/270,973

PRIOR APPLICATION NUMBER: 60/351,908

PRIOR APPLICATION NUMBER: 60/351,908

PRIOR FILING DATE: 2002-01-25

NUMBER OF SEQ ID NOS: 3

SOFTMARE: FastSEQ for Windows Version 4.0

SEQ ID NO 3

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                                                                                                                 TYPE: DNA
TYPE: DNA
ORGANISM: Homo sapiens
PCT-US02-05403-3
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Matches 312; Conserv
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                                                 [100.0%; Score 312; DB 1; milarity 100.0%; Pred. No. 4.le-46; Conservative 0; Mismatches 0;
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| US-60-449-155-36
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| US-10-170-235-38638
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| US-09-946-956-15624
| US-09-468-7258-495
| US-09-471-275-10199
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Sequence 3, Application US/10081817

GENERAL INFORMATION:

APPLICANT: Polyak, Kornelia

APPLICANT: Polyak, Kornelia

APPLICANT: Sgroi, Dennis

APPLICANT: Krop, Ian

TITLE OF INVENTION: HIN-1, A TUMOR SUPPRESSOR GENE

FILE REFERENCE: 00530-094001

CURRENT APPLICATION NUMBER: US/10/081,817

CURRENT FILING DATE: 2002-05-31

PRIOR APPLICATION NUMBER: 60/270,973

PRIOR APPLICATION NUMBER: 60/270,973

PRIOR APPLICATION NUMBER: 60/251,908

PRIOR APPLICATION NUMBER: 60/351,908

PRIOR FILING DATE: 2002-01-25

NUMBER OF SEO ID NOS: 32

SOCTWARE: FastSEQ for Windows Version 4.0

SEO ID NO 3

SEO ID NO 3

LENGTH: 312

TYPE: DNA

ORGANISM: Homo sapiens
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US-10-081-817-3
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Best Local Similarity
Matches 312; Conserv
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                                                                  GAGCTGGGTCCCCAGGCCGTGGGGGCCCTGAAGGCCCTGAAGGCCCTGCTGGGGGGCCCTG
                                                                                                                 CTGAGCAGCCTGGGCATCCCCGTGAACCACCTCATAGAGGGCTCCCAGAAGTGTGTGGCT
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ACAGTGTTTGGC 312
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                                                    GAGCTGGGTCCCCAGGCCGTGGGGGCCCTGAAGGCCCTGAAGGCCCTGCTGGGGGCCCTG
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                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 312; DB 45; ilarity 100.0%; Pred. No. 4.1e-46; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                  Length 312;
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RESULT 3
US-10-631-467-467
US-10-631-467, Application US/10631467
Sequence 467, Application US/10631467
Sequence 467, Application US/10631467
GENERAL INFORMATION:
APPLICANT: Genox Research Inc.
TITLE OF INVENTION: Method for testing for broncheal asthma, or chronic obstructive F
TITLE OF INVENTION: Method for testing for broncheal asthma, or chronic obstructive F
TITLE OF INVENTION: Method for testing for broncheal asthma, or chronic obstructive F
TITLE OF INVENTION: Method for testing for broncheal asthma, or chronic obstructive F
CURRENT FILLE REFERENCE: 3462.1005-000
CURRENT FILLING DATE: 2003-003-00
PRIOR APPLICATION NUMBER: US/10/631,467
CURRENT FILING DATE: 2003-03-20
PRIOR FILING DATE: 2003-03-20
PRIOR FILING DATE: 2003-03-20
PRIOR FILING DATE: 2002-08-06
NUMBER OF SEQ ID NOS: 2086
SOFTWARE: PAtentin version 3.1
SEQ ID NO 467
LENGTH: 461
TYPE: DNA
TYPE: DNA
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US-09-489-036-35171
Sequence 33171, Application US/09489036
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained;
TITLE OF INVENTION From Various Libraries;
FILE REFERENCE: 783
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                                                                       CURRENT APPLICATION NUMBER: US/09/489,036
CURRENT FILING DATE: 2000-01-19
NUMBER OF SEO ID NOS: 35324
SOFTWARE: Hy-patent.pl Version 3.1
SEO ID NO 35171
LENGTH: 446
TYPE: DNA
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Matches 312;
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Best Local
                                                    ORGANISM: Homo sapiens
NAME/KEY: misc_feature LOCATION: (1)...(446)
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322 ACAGTGTTTGGC 333
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Conservative 0;
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Pred. No. 3.9e-46;
); Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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APPLICANT: Hyseq, Inc.
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained
TITLE OF INVENTION: From Various Libraries
FILE REFERENCE: 783
CURRENT EPLICATION NUMBER: US/09/943,143
CURRENT FILING DATE: 2001-08-30
PRIOR APPLICATION NUMBER: 09/489,036
PRIOR FILING DATE: 2000-01-19
NUMBER OF SED ID NOS: 35324
SOFTWARE: Hy-patent.pl Version 3.1
SEQ ID NO 35171
LENGTH: 446
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KSY: misc_feature
LOCATION: (1)...(446)
COCATION: (1)...(446)
COCATION: (1)...(445)
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US-09-943-143-35171
; Sequence 35171, A
; GENERAL INFORMATI
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Best Local Similarity
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Matches
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391 ACAGTGTTTGGC 402
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                                             GAGGCCGGGGCCGGGACCCTGGCCAACCCCCTCGGCACCCTCAACCCGCTGAAGCTCCTG
CTGAGCAGCCTGGGCATCCCCGTGAACCACCTCATAGAGGGCTCCCAGAAGTGTGTGGCT
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Pred. No. 1.
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pred. No. 1.5e-45;
0; Mismatches 2;
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RESULT 7

US-09-710-281-179

Sequence 179, Application US/09710281

GENERAL INFORMATION:
APPLICANT: Hunter, John J.
APPLICANT: Shyjan, Andrew W.
APPLICANT: Stbdal, Hilde
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND TITLE OF INVENTION: THEREFOR FILLE REFERENCE: 1600.2036-001

CURRENT APPLICATION NUMBER: US/09/710,281

CURRENT FILING DATE: 1999-11-09

PRIOR APPLICATION NUMBER: 60/164,254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE 36, Application US/60449155

GENERAL INFORMATION:

APPLICANT: Keith, Tim

APPLICANT: Keith, Tim

FITLE OF INVENTION: NUCLEOTIDE AND AMINO ACID SEQUENCES

FITLE OF INVENTION: RELATING TO RESPIRATORY DISEASES AND C

FILE REFERENCE: HUMO2-11P

CURRENT APPLICATION NUMBER: US/60/449,155

CURRENT FILING DATE: 2003-02-20

NUMBER OF SEQ ID NOS: 1000

SOFTMARE: FastSEQ for Windows Version 4.0

SEQ ID NO 36

LENGTH: 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: DNA; ORGANISM: Human US-60-449-155-36
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US-60-449-155-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 199.0%;
Best Local Similarity 199.4%;
Matches 310; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 308.8; DB 99; Length Pred. No. 1.5e-45; O; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 99; Length 461;
                                                                                  AND
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US-10-170-235-38638
(Sequence 38638, Application US/10170235
(SEQUENCE 38638, Application US/10170235
(GENERAL INFORMATION:
GENERAL INFORMATION: KITS, SUCH AS NUCLEIC ACID ARRAYS, COMPRISING A MAJORITY OF HU
TITLE OF INVENTION: TRANSCRIPTS, FOR DETECTING EXPRESSION AND OTHER USES THEREOF
FILE REFERENCE: C1001380
(CURRENT APPLICATION NUMBER: US/10/170,235
(CURRENT ELLING DATE: 2003-03-17
(NUMBER OF SEQ ID NOS: 42514
(SEQ ID NO 38638
LENGTH: 469

LENGTH: 469
(TYPE: DAM
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Best Local Sir
Matches 310;
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 179
LENGTH: 467
TYPE: DNA
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Best Local :
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352 ACAGTGTTTGGC 363
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                  CTGAGCAGCCTGGGCATCCCCGTGAACCACCTCATAGAGGGCTCCCAGAAGTGTGTGGGCT
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Pred. No. 1.5e-45;
0; Mismatches 2;
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Pred. No. 1.5e-45;
0; Mismatches 2;
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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(491)
; OTHER INFORMATION: n = A,T,C o)
US-09-277-227-11845
RESULT 10
US-09-346-956-15624
US-09-346-956-15624, Application US/09346956
GENERAL INFORMATION:
GENERAL INFORMATION:
ITILE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED ITILE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-758CON1
CURRENT APPLICATION NUMBER: US/09/346,956
CURRENT APPLICATION NUMBER: US/09/346,956
CURRENT APPLICATION NUMBER: US/09/310,298
EARLIER APPLICATION OMBER: US/09/310,298
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US-09-277-227-11845
; Sequence 11845, App
; GENERAL INFORMATION
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CURRENT EPILING DATE: 199-03-25

CURRENT FILING DATE: 199-03-25

NUMBER OF SEQ ID NOS: 23680

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 11845

ENGRH: 491
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Best Local
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mes 310; Conserv
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Pred. No. 1.4e-45;
0; Mismatches 2; Indels 0;
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TYPE: DNA

ORGANISM: Homo sapiens
FEATURE:
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(491)
OTHER INFORMATION: n = A
US-09-904-703-15624
                                                                                                                                                 Sequence 15624, Application US/09904703

GENERAL INFORMATION
APPLICANT: Hyseq, Inc.
ITTILE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBT
ITTILE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-758CON1
CURRENT APPLICATION NUMBER: US/09/904,703
CURRENT FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: 09/210,298
PRIOR FILING DATE: 1998-12-09
NUMBER OF SEQ ID NOS: 17812
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 491
TYPE: DNA
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                                                                                                                                                                                                                                                                                             RESULT 11
US-09-904-703-15624
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Best Local S
Matches 310
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Best Local S
Matches 310
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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 15624
LENGTH: 491
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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310; Conservative
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310; Conserv
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ACAGTGTTTGGC 372
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                                        Score 308.8;
Pred. No. 1.4e
0; Mismatches
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Pred. No. 1.4:
0; Mismatches
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                                    1.4e-45;
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2;
                                                           DB 38;
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Sequence 11845, Application US/09909627

GENERAL INFORMATION:
APPLICANT: HYSeg, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OFF
TITLE OF INVENTION: PROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-766
CURRENT APPLICATION NUMBER: US/09/909.627
CURRENT FILLING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: 09/277,227
PRIOR APPLICATION NUMBER: 09/277,227
PRIOR FILLING DATE: 1999-03-23
NUMBER OF SEQ ID NOS: 23680
SEQ ID NO 11845
LENGTH: 491
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(491)
CURRENT FILLS.
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US-09-909-627-11845
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Best Local S
Matches 310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                       GAGGCCGGGGCCGGGACCCTGGCCAACCCCTCGGCACCCTCAACCCGCTGAAGCTCCTG
                                                                                                                                                                                                                                                  CTGAGCAGCCTGGGCATCCCCGTGAACCACCTCATAGAGGGCTCCCAGAAGTGTGTGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTCTTAGTGGGCTCGGCCAAGCCTGTGGCCCAGCCTGTCGCTGCGCTGGAGTCGGCGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATGAAGCTCGCCGCCCTCCTGGGGCTCTGCGTGGCCCTGTCCTGCAGCTCCGCTCCTCTGTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACAGTGTTTGGC 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAGCTGGGTCCCCAGGCCGTGGGGGCCCGTGAAGGCCCTGAAGGCCCTGCTGGGGGCCCTGCAGGGCCCTGCTGGGGGCCCTGCAGGGCCCTGCTGGGGGCCCTGCAGGCCCTGCTGGAGGCCCTGCAGGCCCTGCAGGCCCTGCTGGAGGCCCTGCTGGAGGCCCTGCTGGAGGCCCTGCTGGGGGCCCTG
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                                                                                                                                        GAGCTGGGTCCCCAGGCCGTGGGGGCCCTGAAGGCCCTGCTGGGGGCCCTGCAGGGCCCTGCTGGGGGCCCTGCAAGGCCCTGCTGGGGGCCCTGCAAGGCCCTGCTGGGGGCCCTGCAAGGCCCTGCTGGGGGCCCTTGAAGGCCCTGCTGGGGGGCCCTTGAAGGCCCTGAAGGCCCTGCTGGGGGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTCTTAGTGGGCTCGGCCAAGCCTGTGGCCCAGCCTGTCGCTGGCGCTGGAGTCGGCGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTGAGCAGCCTGGGCATCCCCGTGAACCACCTCATAGAGGGCTCCCCAGAACTGTGTGGCCT
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                                                                              312
                           372
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Pred. No. 1.4e-45;
0; Mismatches
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GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
APPLICANT: Hyseq, Inc.
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEl Contigs Obtained
TITLE OF INVENTION: NOVEl Contigs Obtained
TITLE OF INVENTION: NOVEl CONTIGS.
CURRENT FILING DATE: 1999-12-23
CURRENT FILING DATE: 1999-01-23
CURRENT FILING DATE: 1999-01-23
CEARLIER APPLICATION NUMBER: US 09/234, 611
EARLIER FILING DATE: 1999-01-22
EARLIER FILING DATE: 1999-01-22
EARLIER FILING DATE: 1999-01-22
EARLIER FILING DATE: 1999-03-25
EARLIER FILING DATE: 1999-03-25
EARLIER FILING DATE: 1999-03-18
EARLIER APPLICATION NUMBER: US 09/271, 490
EARLIER APPLICATION NUMBER: US 09/271, 490
EARLIER FILING DATE: 1999-03-18
EARLIER APPLICATION NUMBER: US 09/274, 861
EARLIER APPLICATION NUMBER: US 09/274, 861
EARLIER APPLICATION NUMBER: US 60/125, 453
EARLIER APPLICATION NUMBER: US 60/125, 453
EARLIER FILING DATE: 1999-03-2
EARLIER APPLICATION NUMBER: US 09/306, 350
EARLIER APPLICATION NUMBER: US 09/306, 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature; LOCATION: (443)...(20)
THER INFORMATION: similar to gi575322 in the genepept database; OTHER INFORMATION: Run with FASTXY 3.3t00, default parameters US-09-471-275-10199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 13
US-09-471-275-10199/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: pt_CT_genes Version 1.0
SEQ ID NO 10199
LENGTH: 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: (1)...(513)
OTHER INFORMATION: n =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                           181
                                                                                                             332
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                                                                                                                                                                                                                              392
                                                                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      310;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                               GAGGCCGGGGCCGGGACCCTGGCCAACCCCCTCGGCACCCTCAACCCGCTGAAGCTCCTG
                       CTGAGCAGCCTGGGCATCCCCGTGAACCACCTCATAGAGGGCTCCCAGAAGTGTGTGGCT
                                                                                                             GAGGCCGGGGCCCGGCCCAACCCCCTCGGCACCCTCAACCCGCTGAAGCTCCTG
                                                                                                                                                                                                                                                             TTCTTAGTGGGCTCGGCCAAGCCTGTGGCCCAGCCTGTCGCTGCGCTGGAGTCGGCGGCG
CTGAGCAGCCTGGGCATCCCCGTGAACCACCTCATAGAGGGCTCCCAGAAGTGTGTGGCT
                                                                                                                                                                                                                                 TTCTTAGTGGGCTCGGCCAAGCCTGTGGCCCAGCCTGTCGCTGGGCTGGAGTCGGCGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 308.8; DB 21;
Pred. No. 1.4e-45;
0; Mismatches 2;
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0;

Gaps

240

273

213

180

333 120 393 60 release 114

QY

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Sequence 495, Application US/09488725B
GENERAL INFORMATION:
APPLICANT: Yuanhua T. Tang
APPLICANT: John Tillinghast
APPLICANT: Ankura Sinku
APPLICANT: Chenghua Liu
APPLICANT: Chenghua Liu
APPLICANT: Radoje T. Drmanac
TITLE OF INVENTION: Novel Contigs Obtained
TITLE OF INVENTION: From Various Libraries
FILE REFERENCE: 784
                                                                                                                                                                                                  PEATURE:

NAME/KEY: misc_feature

LOCATION: (1)...(513)

OTHER INFORMATION: n = a,t,c or g

FEATURE:

NAME/KEY: misc_feature

LOCATION: (75)...(496)

OTHER INFORMATION: similar to gi575322 in the genepept database release 114,

OTHER INFORMATION: Run with FASTXY 3.3t00, default parameters

US-09-488-725B-495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/488,725B
CURRENT ETLING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US 09/004,182
PRIOR FILLING DATE: 1998-01-07
PRIOR FILLING DATE: 1998-02-13
PRIOR FILLING DATE: 1998-02-13
PRIOR PRICING DATE: 1998-02-13
PRIOR PRICING DATE: 1998-03-20
PRIOR PRICING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: US 09/321,214
PRIOR APPLICATION NUMBER: US 09/321,214
PRIOR APPLICATION NUMBER: US 09/31,598
PRIOR FILLING DATE: 1998-08-10
PRIOR PRICING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: US 09/170,294
PRIOR APPLICATION NUMBER: US 09/179,473
PRIOR APPLICATION NUMBER: US 09/179,473
PRIOR APPLICATION NUMBER: US 09/181,430
PRIOR APPLICATION NUMBER: US 09/181,430
PRIOR APPLICATION NUMBER: US 09/235,076
PRIOR APPLICATION NUMBER: US 09/235,076
PRIOR APPLICATION NUMBER: US 09/234,611
PRIOR FILING DATE: 1999-01-20
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US-09-488-725B-495
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                                                                                                                                                                                                                                                                                                                                                                                                        Remaining Prior Application data removed
NUMBER OF SEQ ID NOS: 10289
SOFTWARE: pt_CT_genes Version 1.01
SEQ ID NO 495
LENGTH: 512
                                                                                                                                     Matches
                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
 301
                                                                  61
                                                                                                                                 al Similarity 99.4
310; Conservative
                                                                GAGCTGGGTCCCCAGGCCGTGGGGGCCGTGAAGGCCCTGAAGGCCCTGCTGGGGGCCCTG 300

GAGCTGGGTCCCCAGGCCGTGGGGGCCCTGAAGGCCCTGAAGGCCCTGCTGGGGGCCCTG 153
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                                                                                                                                                 99.0%;
                                                                                                                                   0;
                                                                                                                               Score 308.8; DB 21.
Pred. No. 1.4e-45;
D; Mismatches 2;
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                                                                                                                                                                   21;
                                                                                                                                   Indels
                                                                                                                                                                 Length 512;
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                                   120
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US-08-791-710-4
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                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 518 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/08791710
GEMERAL INFORMATION:
GEMERAL INFORMATION:
APPLICANT: RUSSell, John C.
APPLICANT: Colpitts, Tracey L.
TITLE OF INVENTION: REAGENTS AND METHODS FOR DETECTING
TITLE OF INVENTION: LUNG DISEASES
UMMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: About Laboratories, D377/AP6D
STREET: 100 Abbott Park Road
                                                                                                                                   Query Match
Best Local S
Matches 310
                                                                                                                                                                                                                                                                                                                                               STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: ILM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/791,71
FILING DATE:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION UMBER: US/08/791,71
FILING DATE:
FILING DATE:
FILING DATE:
APPLICATION DATA:
APPLICATION UMBER: 33207
REFERENCE/DOCKET NUMBER: 5998.US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-937-0378
                                                                                                                                                                                                                                                                                                                                         TELEFAX:
   139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    361
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                                   61
                                                                  79
                                                                                                                                   il Similarity
310; Conser
                                                                ACAGTGTTTGGC 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAGCTGGGTCCCCAGGCCGTGGGGGGCCCTGAAGGCCCTGAAGGCCCTGCTGCTGCGGGGCCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAGCTGGGTCCCCAGGCCGTGGGGGCCCTGAAAGGCCCCTGCTGGGGGGCCCTG
                                                                                                                                                                                                                                                                                                                                        847-938-2623
                                                                                                                                   Conservative
                                                                                                                                                 99.08;
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                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                         5998.US
                                                                                                                               Score 308.8; DB 12;
Pred. No. 1.4e-45;
0; Mismatches 2;
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                                                                                                                                                                 Length
                                                                                                                                                                 518;
                                                                                                                                   0;
                                                                                                                                 Gaps
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| · | rch completed: September | 121 GAGGCCGGGGCCG                                          |
|---|--------------------------|------------------------------------------------------------|
|   | 20, 2003, 03:12:33       | GAGGCCGGGGACCCTGGCCAACCCCTCGGCACCCTCAACCCGCTGAAGCTCCTG 180 |

nucleic

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Title:
Perfect score:
Sequence:
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
  Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               September 20, 2003, 00:35:14; Search time 61.46 Seconds (without alignments) 4337.104 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-081-817A-3
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Match Length
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// cgn2_6/ptodata/1/pna/PcT_NEW_COMB.seq:*

// cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq:*

// cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq:*

// cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:*

// cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:*

// cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:*

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SUMMARIES
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         e 19, Appl
e 25275, Ap
e 1736, Ap
e 31483, A
e 28647, A
e 1081, Appl
e 1081, Appl
e 30728, A
e 25485, A
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Sequence 3. Application

GENERAL INFORMATION:

APPLICANT: Polyak, Kornelia
APPLICANT: Porter, Dale
APPLICANT: Porter, Dale
APPLICANT: Sgroi, Dennis
APPLICANT: Strop, Ian
TITLE OF INVENTION: HIN-1, A TUMOR SUPPRESSOR GEN
FILE REFERENCE: 00530-094001
FILE REFERENCE: 00530-094001
CURRENT APPLICATION NUMBER: US/10/081,817A
CURRENT FILING DATE: 2002-02-22
PRIOR APPLICATION NUMBER: US 60/270,973
PRIOR APPLICATION NUMBER: US 60/351,908
PRIOR APPLICATION NUMBER: US 60/270,973
PRIOR APPLICATI
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US-60-494-568-16
US-10-425-114A-23253
US-10-425-114A-30359
US-60-487-610-31
US-60-487-610-32
US-10-425-114A-147
US-10-355-238-1
US-10-425-114A-1737
US-10-425-114A-24020
US-10-425-114A-24020
US-10-369-983-8
US-10-369-983-8
US-10-369-983-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 312;
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Sequence 15, Appl
Sequence 33253, A
Sequence 30359, A
Sequence 31, Appl
Sequence 32, Appl
Sequence 1447, Appl
Sequence 147, Appl
Sequence 1737, Ap
Sequence 1737, Ap
Sequence 21616, A
Sequence 21616, A
Sequence 4, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 5, Appli
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60

240 180 180 Result No.

O

В

Length 252 Indels

180

120 60

0

240 300 180 240 120

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APPLICANT: POIYAK, KOTNELIA
APPLICANT: POITER, Dale
APPLICANT: SGROI, Dennis
APPLICANT: SGROI, Dennis
ITILE OF INVENTION: HIN-1, A TUMOR SUPPRESSOR GENE
FILE REFERENCE: 00530-094001
CURRENT APPLICATION NUMBER: US/10/081,817A
CURRENT APPLICATION NUMBER: US 60/270,973
PRIOR APPLICATION NUMBER: US 60/270,973
PRIOR FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: US 60/351,908
PRIOR FILING DATE: 2001-02-3
PRIOR FILING DATE: 2001-03-23
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 23
LENGTH: 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: POLYAK, KOTDELIA

APPLICANT: SGROI, Dennis

APPLICANT: SGROI, Dennis

APPLICANT: KTOP, IDENNis

TITLE OF INVENTION: HILN-1, A TUMOR SUPPRESSOR GENE

FILE REFERENCE: 00530-094001

CURRENT APPLICATION NUMBER: US/10/081,817A

CURRENT FILING DATE: 2002-02-22

PRIOR APPLICATION NUMBER: US 60/270,973

PRIOR APPLICATION NUMBER: US 60/351,908

PRIOR APPLICATION NUMBER: US 60/351,908

PRIOR FILING DATE: 2002-01-25

NUMBER OF SEQ ID NOS: 32

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 4

LENGTH: 258

TYPE: DNA
                                                                                                                                                                                                                                                                      RESULT 3
US-10-081-817A-23
Sequence 23, Application US/10081817A
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 2
US-10-081-817A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/10081817A GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                       181
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                                                                                                                                                                                                                                                                                                                                                                                                                                     GTGGCTGAGCTGGGTCCCCAGGCCGTGGGGGCCGTGAAGGCCCTGAAGGCCCTGCTGGGG
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US-10-081-817A-7

Sequence 7, Application US/10081817A

GENERAL INFORMATION:
APPLICANT: Polyak, Kornelia
APPLICANT: Porter, Dale
APPLICANT: Sgroi, Dennis
APPLICANT: Sgroi, Dennis
APPLICANT: Sgroi, Dennis
APPLICANT: Krop, Ian
ITILE OF INVENTION: HIN-1, A TUMOR SUPPRESSOR GENE
FILE REFERENCE: 00530-094001
CURRENT APPLICATION NUMBER: US/10/081,817A
CURRENT FILING DATE: 2002-02-22
PRIOR APPLICATION NUMBER: US 60/270,973
PRIOR APPLICATION NUMBER: US 60/270,973
PRIOR APPLICATION NUMBER: US 60/351,908
PRIOR FILING DATE: 2002-01-25

NUMBER OF SEO ID NOS: 32
SOFTWARE: FASTSEQ FOR Windows Version 4.0
SEQ ID NO 7
LENGTH: 312
TYPE: DNA
ORGANISM: Mus musculus
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                                                                                                                                                                                                                                                                        Ouery Match 34.7%; Score 108.2; DB 6; Length 312; Best Local Similarity 65.7%; Pred. No. 2.6e-15; Matches 190; Conservative 0; Mismatches 93; Indels 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 252; Conserva
                   192
                           183 GAGCAGCCTGGGCATCCCCGTGAACCACCTCATAGAGGGCTCCCAGAAGTGTGTGGGCTGA 242
                                                                                 132
                                                                                                126 CGGGGCCGGGACCCTGGCCAAC----CCCCTCGGCACCCCTCAACCCGCTGAAGCTCCTGCT 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72 GGACTCATTGGCCAAGCCTGCGGTAGAACCCGTGGCCGCTTGCTCCAGCTGCAGAGGC
                                                                                                                                                            69 GGCCTC---GGCCAAGCCTGTGGCCCAGCCTGTGGGTGGAGTCGGCGGAGGC
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5.2e-47;
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APPLICANT: POTTER: Dale
APPLICANT: STOI, Dale
APPLICANT: STOI, Dale
APPLICANT: STOI, Dale
APPLICANT: STOI, Dale
TITLE OF INVENTION: HIN-1, A TUMOR SUPPRESSOR GENE
TITLE REFERENCE: 00530-094001
CURRENT APPLICATION NUMBER: US/10/081,817A
CURRENT FILING DATE: 2002-02-22
PRIOR APPLICATION NUMBER: US 60/270,973
PRIOR APPLICATION NUMBER: US 60/270,973
PRIOR FILING DATE: 2001-02-23
PRIOR FILING DATE: 2002-01-25
NUMBER OF SEO ID NOS: 32
SOFTWARE: FASTSEO for Windows Version 4.0
SEO ID NO 25
SEO ID NO 25
                                            Sequence 8, Application US/10081817A

GENERAL INFORMATION:
APPLICANT: POLYAK, Kornelia
APPLICANT: POLYAK, Cornelia
APPLICANT: SGTO1, Dale
APPLICANT: SGTO1, Dale
TITLE OF INVENTION: HIN-1, A TUMOR SUPPRESSOR GENE
TITLE OF INVENTION: HIN-1, A TUMOR SUPPRESSOR GENE
CURRENT FILLING DATE: 2002-02-22
PRIOR APPLICATION NUMBER: US 60/270,973
PRIOR APPLICATION NUMBER: US 60/270,973
PRIOR APPLICATION NUMBER: US 60/351,908
PRIOR APPLICATION NUMBER: US 60/351,908
PRIOR APPLICATION NUMBER: US 60/351,908
PRIOR FILING DATE: 2002-01-25
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 255
TYPE: NAM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: DNA; ORGANISM: Mus musculus US-10-081-817A-25
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; TYPE: DNA; ORGANISM: Mus musculus US-10-081-817A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          178 CTGCTGAGCAGCCTGGGCATCCCCGTGAACCACCTCATAGAGGGCTCCCCAGAAGTGTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 GAGGCCGGGGCCGGGACCCTGGCCAACCCCC---TCGGCACCCTCAACCCGCTGAAGCTC 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64 GAGGCTGTGGCAGGGGCTGTGCCTAGCCTACCATTAAGCCACTTGGCCATCCTGAGGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCGAGCTGGGCCCTGAGGCTGTAGGAGCTGTGAAGTCACTGCTGGGGGGTCCTG 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCTGAGCTGGGTCCCCAGGCCGTGGGGGCCCTGAAGGCCCTGAAGGCCCTGCTG 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28.8%;
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Pred. No. 2.6e-11;
); Mismatches 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     123
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Sequence 20. Application US/10081817A

[GENERAL INFORMATION:
APPLICANT: Polyak, Kornelia
APPLICANT: Polyak, Kornelia
APPLICANT: Polyak, Consis
APPLICANT: SGroi, Dale
ITILE OF INVENTION: HIN-1, A TUMOR SUPPRESSOR GENE
FILE REFERENCE: 00530-094001
[CURRENT PILING DATE: 2002-02-22
[CURRENT FILING DATE: 2002-02-22
[PRIOR APPLICATION NUMBER: US 60/270,973
[PRIOR APPLICATION NUMBER: US 60/270,973
[PRIOR APPLICATION NUMBER: US 60/351,908
[PRIOR FILING DATE: 2002-01-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Д
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US-10-081-817A-20
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Best Local Simi
Matches 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: DNA; ORGANISM: Rattus norvegicus US-10-081-817A-20
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RESULT 8
US-10-081-817A-26
US-10-081-817A-26
Sequence 26, Application US/10081817A
GENERAL INFORMATION:
APPLICANT: Polyak, Kornelia
APPLICANT: Porter, Dale
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Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 GAGGCCGGGGGCCGGGACCCTGGCCAACCCCC---TCGGCACCCTCAACCCGCTGAAGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   190 ACCGAGCTGGGCCCTGAGGCTGTAGGAGCTGTAAGTCACTGCTGGGGGTCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     238 GCTGAGCTGGGTCCCCAGGCCGTGGAGGCCCTGAAGGCCCTGCTG 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 TTCTTAGTGGGCTCGGCCAAGCCTGTGGCCCAGCCTGTCGCCTGGAGTCGGCGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 TTCATGGACTCATTGGCCAAGCCTGCGGTAGAACCCGTGGCCGCCCTTGCTCCAGCTGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     135 GACCCTGGCCAACCCCC---TCGGCACCCTCAACCCGCTGAAGCTCCTGCTGAGCAGCCT 191
                                                                                                                                                                                                                                                                                                                                                                  108 GGCTGTGCCTAGCCTACCATTAAGCCACTTGGCCATCCTGAGGTTCATCGTGACCAGCCT 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAGGCTGTGGCAGGGGCTGTGCCTAGCCTAGCCATTAAGCCACTTGGCCATCCTGAGGTTC
                                                                                                                                                                                                              CCAGGCCGTGGGGGCCCTGAAGGCCCTGCTG 291
                                                                                                                                                                                                                                                                                                                          GGGCATCCCATTGGATCCTCATAGATGGTTCCAGGAAGTGCGTCACCGAGCTGGGCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 87.4; DB 6;
Pred. No. 9.8e-11;
0; Mismatches 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 279;
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I APPLICANT: Krop, Ian
I TITLE OF INVENTION. HIN-1, A TUMOR SUPPRESSOR GENE
ITILE PRIFERENCE: 00530-094001
CURRENT APPLICATION NUMBER: US/10/081,817A
CURRENT FILING DATE: 2002-02-22
PRIOR APPLICATION NUMBER: US 60/270,973
PRIOR APPLICATION NUMBER: US 60/270,973
PRIOR FILING DATE: 2001-02-3
PRIOR APPLICATION NUMBER: US 60/351,908
PRIOR APPLICATION NUMBER: US 60/351,908
PRIOR APPLICATION NUMBER: US 60/351,908
PRIOR FILING DATE: 2002-01-25
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 249
                                                                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: HSV2
PCT-US03-11231-193
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; Sequence 193, Application
; GENERAL INFORMATION;
; APPLICANT: CORTIAN COMPORT
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                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                        Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                        APPLICANT: Day, Craig H.

APPLICANT: Hosken, Nancy A.

APPLICANT: PATSONS, JOSEPH M.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND TITLE OF INVENTION: TREATMENT OF HERPES SIMPLEX VIRUS INFECTION CURRENT FILE REFERENCE: 210121.53801PC

CURRENT FILING DATE: 2003-04-09

NUMBER OF SEQ ID NOS: 267

SOFTWARE: FASTLING DATE: 2003-04-09

                                                                                                                                                                                                                                                                                                               TYPE: DN
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                                      1981 GCCGTGCCGGGCCGGAGCCCGGCGCCCCCCGCGCGCCCCGGGGCCCGCGGGC
127 GGGGCCGGGACCCTGGCCAACCCCCTCGGCACCCTCAACCCGCTGAAGCTCCTGCTGAGC 186
                                                                                                                                                                                                al Similarity
142; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              198 TGAGGCTGTAGGAGCTGTGAAGTCACTGCTGGGGGGCCCCTG 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   252 CCAGGCCGTGGGGGCCCTGAAGGCCCTGAAGGCCCTGCTG 291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTGGCCGCCTGCCGCGGATCCTGGAGGCGCTGGCGGAGGGCTTCGACGGCGACCTGGCG 1980
                                                                                                                                    CTCGCCGCCTCCTGGGGCTCTGCGTGGCTCGTGCTTTCTTA
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                                                                                                                                                                                            0,
                                                                                                                                                                                      Score 50.8; DB 1;
Pred. No. 0.017;
0; Mismatches 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 87.2; DE Pred. No. 1.1e-0; Mismatches
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..le-10;
hes 73;
                                                                                                                                                                                                                          Length 3957;
                                                                                                                                                                                      Indels
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RESULT 11
US-60-487-610-740
; Sequence 740, Application US/60487610
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: HUANG, Hongjin
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CURRENT ETLING DATE: 2001-04-25
PRIOR APPLICATION NUMBER: US 09/599,362
PRIOR FILLING DATE: 2000-06-21
PRIOR PPLICATION NUMBER: US 60/141,032
PRIOR PPLICATION NUMBER: US 60/141,032
PRIOR FILLING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: US 60/1699/02058
PRIOR APPLICATION NUMBER: US 09/469,099
PRIOR FILLING DATE: 1999-12-20
PRIOR FILLING DATE: 1999-12-21
PRIOR FILLING DATE: 1999-13-21
PRIOR APPLICATION NUMBER: US 60/113,686
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US-09-842-364A-10
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Best Local S
Matches 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US (
PRIOR FILING DATE: 1998-12-22
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PATENTIN VERSION 3.2
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 10, Application US/09842364A
GENERAL INFORMATION:
APPLICANT: Yen-Potin, Frances
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Apolipoprotein A-IV-related Protein: Polypeptide, TITLE OF INVENTION: Sequences and Biallelic Markers Thereof FILE REFERENCE: G-089US04CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Human
                                                                                                                                                  1002
                                                                                                                                                                                                        258
                                                                                                                                                                                                                                    198 CCCCGTGAACCACCTCATAGAGGGCTCCCAGAAGTGTGTGGCTGAGCTGGGTCCCCAGGC 257
                                                                                                                                                                                                                                                                        138 CCTGGCCAACCCCCTCGGCACCCTCAACCCGCTGAAGCTCCTGCTGAGCAGCCTGGGCAT
                                                                                                                                                                                                                                                                                                                                            822 CCAGCTTGAGGGCCTGACCTTCCAGATGAAGAAGAACGCCGAGGAGCTCAAGGCCAGGAT
                                                                                                                                                                                                                                                                                                                                                                                                                        110; Conserv
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                                                                                                                                                                        CGTGGGGGCCGTGAAGGCCCTGCTGGGGGGCC 297
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Denison, Blake
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Bouguelert, Lydie
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Dumas Milne Edwards, Jean-Baptiste
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Bihain, Berna
                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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Sequence 7, Application US/09475704A

GENERAL INFORMATION:

APPLICANT: Barnett, Susan

APPLICANT: Zur Megede, Jan

TITLE OF INVENTION: POLYNEDTIDES ENCODING ANTIGENIC HIV TYPI

TITLE OF INVENTION: POLYNEDTIDES, POLYPEPTIDES AND USES THERE

FILE OF INVENTION: POLYPEPTIDES, POLYPEPTIDES AND USES THERE

CURRENT APPLICATION NUMBER: US/09/475,704A

CURRENT FILING DATE: 1999-12-30

PRIOR APPLICATION NUMBER: 60/152,195

PRIOR APPLICATION NUMBER: 60/152,195

PRIOR FILING DATE: 1999-01

NUMBER OF SEQ ID NOS: 30

SOFTWARE: PALENTIN Ver. 2.0

LENGTH: 1944

TYPE: NNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Homo sapiens US-60-487-610-740
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                                                                                                                                                                                                      ; OTHER INFORMATION: Description of Artificial Sequence: ; OTHER INFORMATION: gpl40 coding region of HIV strain Al US-09-475-704A-7
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US-09-475-704A-7
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Best Local S
Matches 132
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TITLE OF INVENTION: LIVER FIBROSIS IN HERATITIS C VIRUS-INFECTED SUBJECTS,
TITLE OF INVENTION: METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001469
CURRENT FILLING DATE: 2003-07-17
NUMBER OF SEQ ID NOS: 97101
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 740
LENGTH: 1754
                                                                                                                                Matches
                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                             LENGTH: 1944
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                      1377
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CCAGCCTGTCGCTGGGGTCGGAGTCGGCGGGGGCGGGGGCCGGGGGCCGGGGCCGACCCC
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                                                      CCTGGGCGTGGCCCCCCCCGAGGGGCCCAAGCGCCGCGTGGTGGAGCGCGAGAAGCGCGCCGT
                                                                                         CGTGGCCCTGTCCTGCAGCTCCGCTCGTGCTTTCTTAGTGGGCTCGGCCAAGCCTGTGGC
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                                                                                                                                Conservative
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Pred. No. 0.53;
1; Mismatches 148;
                                                                                                                              Score 43.8; DI Pred. No. 0.54.0; Mismatches
                                                                                                                                             .54;
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                                                                                                                                Indels
                                                                                                                                                                                                                            e: synthetic
AF110968
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Sequence 739, Application US/60487610

GENERAL INFORMATION:
APPLICANT: CARCILL, Michele
APPLICANT: CARCILL, Michele
APPLICANT: HOANG, HONGJIN
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001469
FILE REFERENCE: CL001469
CURRENT APPLICATION NUMBER: US/60/487,610
CURRENT FILIG DATE: 2003-07-17
NUMBER OF SEQ ID NOS: 97101
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 739
LENGTH: 2425
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US-09-475-704A-8
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US-60-487-610-739
Sequence 8, Application US/09475704A

GENERAL INFORMATION:
APPLICANT: Barnett, Susan
APPLICANT: Zur Megede, Jan
TITLE OF INVENTION: POLYNGCLEOTIDES ENCODING ANTIGENIC
TITLE OF INVENTION: POLYPEPTIDES, POLYPEPTIDES AND USE
FILE REFERENCE: 1631.002
FILE REFERENCE: 1631.002
CURRENT APPLICATION NUMBER: US/09/475,704A
CURRENT FILING DATE: 1999-12-30
PRIOR APPLICATION NUMBER: 60/152,195
PRIOR FILING DATE: 1999-09-01
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Best Local S
Matches 132
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132; Conserv
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                                                                                                                                                                                                                                                                                                                                                                           CAGCCTGGGCATCCCCGTGAACCACCTCATAGAGGGCTCCCAGAAGTGTGTGGCTGAGCT 245
                                                                                                                                                                                                                                                                                                                                                                                                                     CGGGGTCCGGGAGGTGCCGMAGGCCCTAAGGGACCAGGGTATTGCAGGTTCCGACGGT 1344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGCAGCATGGGAGACCCCGGCCTTCCAGGCCCCCAGGGCCTCCGAGGTGACGTGGGCGAC 1284
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ilarity 47.0%;
Conservative
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Pred. No. 0.56;
l; Mismatches 148;
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                                                                                               AND USES
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CURRENT FILING DATE: 2003-07-17
NUMBER OF SEQ ID NOS: 97101
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 738
LENGTH: 2480
TYPE: DNA
ORGANISM: Homo sapiens
US-60-487-610-738
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US-60-487-610-738
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; TYPE: DNA
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: gp160 coding region of HIV strain AF110968
us-09-475-704A-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 738, Application US/60487610
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
APPLICANT: HUANG, Hongjin
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,
TITLE OF INVENTION: METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001469
                                                                                                                                                                                                                                                                                 Query Match 14.0%;
Best Local Similarity 47.0%;
Matches 132; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 129; Conserv
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SOFTWARE: PatentIn Ver.
SEQ ID NO 8
LENGTH: 2466
                                                                                                                                                                                               1165 GCCCTCGGCCCACAAGGCCCCTCCCGGAGCCCCTGGTGTCCGAGGCCTTCCAGGGCCAGAAG 1224
                                     1285 CGGGGTCCGGGAGGTGCCGMAGGCCCTAAGGGAGACCAGGGTATTGCAGGTTCCGACGGT 1344
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                                                                                                                    1225 GGCAGCATGGGAGACCCCGGCCTTCCAGGCCCCCAGGGCCTCCGAGGTGACGTGGGCGAC
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                                                                                                                                                                                                                                       6 GCTCGCCGCCCTCTGGGGCTCTGCGTGCCTGTCCTGCAGCTCCGCTCGTGCTTTCTT 65
                                                                             CGGGGCCGGGACCCTGGCCAACCCCTCGCCAACCCGCTGAAGCTCCTGCTGAG 185
                                                                                                                                                          AGTGGGCTCGGCCAAGCCTGTGGCCCAGCCTGTCGCTGGAGTCGGCGGCGGAGGC 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAGCATCACCCTGACCGTGCAGGCCCGCCTGCTGCTGAGCGGCATCGTGCAGCAGCAGAA
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Pred. No. 0.56;
1; Mismatches 148; Indels
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Search completed: September 20, 2003, 03:15:36 Job time: 64.46 secs

Дb

1405 GGCAGTCGAGGGGAGCTGGGCCCCAAAGGCACCCAGGGTCC 1445

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Database :
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Searched:
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Gapop 10.0 , Gapext 1.0
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312
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gb_in:*
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em_htgo_hum:*
em_htgo_mus:*
em_htgo_other:*
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Pred. No. is the number of results predicted by chance to have

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

## Result No. 108.2 90.4 90.4 90.4 % Query Match 100.0 1948 106873 156789 93872 853 147774 237987 303550 33557 154746 154746 154746 154746 166644 523 589 245659 283593 630 254981 347 130129 166777 168347 190024 127488 Length DB 10 10 10 9 9 AC131456 AC131437 AC131457 AC131457 AC131457 AC1313457 AC1313457 AC1313457 AC3131455 AX376176 BC024232 AC0114867 AF274961 AF274961 AC106616 AC10661 BD082141 AX201348 AX252648 AX403520 AX7313458 AC106813 AC106813 AC025336 AC122714 AC025336 BD082139 BX334451 AY040564 HUMZB52D10 BC029176 BD082142 BD082138 AY040564 Homo sapi AF086152 Homo sapi BC029176 Homo sapi BC029176 Homo sapi BD082141 Reagents AX201348 Sequence AX201348 Sequence AX201348 Sequence AX201348 Homo sapi AC106813 Homo sapi AC106813 Homo sapi AC022095 Homo sapi AC022095 Homo sapi BD082119 Reagents AX334451 Sequence BD082138 Reagents AX33451 Sequence BD082137 Rattus no AC1313457 Mus muscu AC098957 Rattus no AC131433 Rattus no AC131433 Rattus no AC131437 Mus muscu AC098957 Mus muscu AC098957 Mus muscu AC098957 Rattus no AF313457 Homo sapi AC0124222 Homo sapi AC0142867 Mus muscu AC104867 Homo sapi AC01152 Homo sapi AC01154 Homo sapi AC01154 Homo sapi AC01224 Homo sapi AF289024 Homo sapi AF289026 Cercopith AF33748 Cercopith Description

## ALIGNMENTS

|                                                                                                                                                                                  | AUTHORS                                                      |                                                            |                                                                   | ORGANISM     | SOURCE               | KEYWORDS | VERSION                | ACCESSION  | DEFINITION                                               | Locus                                       | AY040564 | RESULT 1 |
|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------|------------------------------------------------------------|-------------------------------------------------------------------|--------------|----------------------|----------|------------------------|------------|----------------------------------------------------------|---------------------------------------------|----------|----------|
| Seth, P., Kaelin, C.M., Rhei, E., Bosenberg, M., Schnitt, S., Seth, P., Kaelin, C.M., Rhei, E., Bosenberg, M., Schnitt, S., Seth, P., Kaelin, C.M., Razumovic, J. and Polyak, K. | Krop.T.F., Sqroi.D., Porter.D.A., Lunetta.K.L., LeVangie.R., | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | Homo sapiens | Homo sapiens (human) |          | AY040564.1 GI:15079187 | AY040564 - | Homo sapiens HIN-1 putative cytokine mRNA, complete cds. | AY040564 461 bp mRNA linear PRI 15-AUG-2001 |          |          |

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ACCESSION
VERSION
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312; Conserv
Homo sapiens (human)
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Obases 1 to [471]
Woessner, J., Tan, F., Marra, M., Kucaba, T., Yandell, M., Martin, J.,
Marth, G., Bowles, L., Wylie, T., Bowers, Y., Steptoe, M., Theising, B.
Geisel, S., Allen, M., Underwood, K., Chappell, J., Person, B.,
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cancerous mammary e
Proc. Natl. Acad. S
21396515
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Homo sapiens full length
AF086152
AF086152.1 GI 3483497
FLI_CDNA.
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Polyak,K., Krop,I. and Sgroi,D.
Direct Submission
Submitted (15-JUN-2001) Adult Oncology,
Submitted (15-JUN-2001) BJ40C, Boston,
Institute, 44 Binney St. DJ40C, Boston,
                                                                                                                                                                                                                                  GAGCTGGGTCCCCAGGCCGTGGGGGCCCTGAAGGCCCTGAAGGCCCTGCTGGGGGGCCCTG
                                                                                                                                                                                                                                                                             CTGAGCAGCCTGGGCATCCCCGTGAACCACCTCATAGAGGGCTCCCAGAAGTGTGTGGCT
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ilarity 100.0%;
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/molltype="mRNA"
/db_xref="taxon:9606"
/chromosome="5"
/map="5935-tel"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="HIN-1 putative cytokine"
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/db_xref="GI:15079188"
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GT_AAPLGTLNPLKLLLSSLGIPVNHLIEGSQKCVAELGPQAVGAVKALKALLGALTV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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Pred. No. 1.8e-39;
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cDNA clone
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MA 02115, USA
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ZB52D10.
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Department of Genetics
washington University
St. Louis MO 63108, USA
http://genome.wustl.edu/gsc
mailto:est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTICE: This sequence represents the full insert of this cDNA. At attempt has been made to verify whether this corresponds to the full-length of the original mRNA from which it was derived. We have tried to obtain double-stranded, or double chemistry sequence across the entire clone, but potentially, there are areas in the sequence where this level of coverage was not achieved. Nevertheless, we are confident of the accuracy of this sequence as all regions of low quality, as defined by PHRAP (P. Green, in preparation), were visually inspected and edited accordingly. The consensus quality values for this sequence have been submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Waterston,R.
Direct Submission
Submitted (24-AUG-1998) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
SUBMITTED BY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gibbons,M., Harvey,N., Pape,D., Chamberlain,A., Morales,R., Schurk,R., Ritter,E., Kohn,S., Swaller,T., Behymer,K., Hillier,L., Wilson,R. and Waterston,R. Full Clone Sequencing of the Longest Available Member from Each Unigene Cluster Unpublished 2 (bases 1 to 471)
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                   ACAGTGTTTGGC 312
                                                                                                                                                           CTGAGCAGCCTGGGCATCCCCGTGAACCACCTCATAGAGGGCTCCCAGAAGTGTGTGGCT
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:307219"
/clone=lib="Soares_fetal_lung_NbHL19W"
/ 171 c 149 g 73 t
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NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Sequencing by: Baylor College of Medicine Human Genomu
Sequencing Center
Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          503 bp mRNA linear PRI 16-MAY-2002 Homo sapiens, secretoglobin, family 3A, member 1, clone MGC:34758 IMAGE:5180304, mRNA, complete cds.
  121
                                                                                                                                                                            al Similarity 99.4
310; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (01-MAY-2002) National Institutes of Health, Mammalian Submitted (01-MAY-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 503)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINI at: http://image.llnl.gov Series: IRAK Plate: 50 Row: b Column: 24
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Genomescan gene prediction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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                                  76
                                                             61
                                                                                                      16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Web site: http://www.hgsc.bcm.tmc.edu/cdna/Contact: amg@bcm.tmc.edu
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., García, A.M., Lu, X., Huly.
Yoon, V.S., Kowis, C.R., Lawrence, S., Mart
Richards, S., Gibbs, R.A.
                                                                                                                                         بسا
                                                                                                    GAGGCCGGGGCCCTGGCCAACCCCCTCGGCACCCTCAACCCGCTGAAGCTCCTG 180
                                                                                                                                                                                                                                                                  116
                                                                                                                                                                                                                                                                                             /product="secretoglobin, family 3A, member 1"
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/clone_lb="NIH_MGC_115"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                  EG
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                                                                                                                                                                          score 308.8; DB 9;
Pred. No. 5.5e-39;
); Mismatches 2;
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Martin,
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1 (bases 1 to 51)

1 (bases 1 to 51)

1 (bases 1 to 50)

1 (Cohen, M., Colpitts, T.L., Friedman, P.N., Gordon, J., Medel, P.A.B., Cohen, M., Colpitts, T.L., Kratochvil, J.D., Rapp, L.R., Russell, J.C. and Stroupe, S.D.

Russell, J.C. and Stroupe, S.D.

Reagents and methods useful for detecting diseases of the lung Patent: JP 200152225-A 6 13-NOV-2001; ABBOTT LABORATORIES
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BD082142.1 GI:22627752
JP 2001522225-A/6.
                                                                                                    61 TTCTTAGTGGGCTCGGCCAAGCCTGTGGCCCAGCCTGTCGCTGCGCTGGAGTCGGCGGGG
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C Topology: Linear;
                                GAGGCCGGGGCCGGGACCCTGGCCAACCCCCTCGGCACCCTCAACCCGCTGAAGCTCCTG 180
                                                                                    TTCTTAGTGGGCTCGGCCAAGCCTGTGGCCCAGCCTGTCGCTGCGCTGGAGTCGGCGGCG
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                                                                                                                                                                                                                                                                                                                 78
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C12N15/63,C12N5/10,C12Q1/68,C07K14/47//C07K16/30,G01N33/574 CC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JON D KRATOCHVIL, LISA ROBERTS RAPP, JOHN C RUSSELL, STEPHEN D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PATRICIA A BILLING MEDEL, MAURICE COHEN, TRACEY L COLPITTS, PAULA
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31-JAN-1997 US 08/791710
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13-NOV-2001
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1. .519
                                                                                                                                                                                                                                                                                                               /organism="Zea mays"
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190 c 170 g
                                                                                                                                                                                                                                           99.08;
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Pred. No. 5.
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138 60

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1 (bases 1 to 562)

Redel, P.A.B., Cohen, M., Colpitts, T.L., Friedman, P.N., Gordon, J., Granados, E.N., Hodges, S.C., Klass, M.R., Kratochvil, J.D., Rapp, L.R., Russell, J.C. and Stroupe, S.D.

Reagents and methods useful for detecting diseases of the lung Patent: JP 2001532225-A 5 13-NOV-2001;

ABBOTT LABORATORIES
PN JP 200152225-A/5
PD 13-NOV-2001
PT 30-JAN-1998 JP 1998533078
PR 31-JAN-1999 US 08/791710
PI PATRICIA, A BILLING MEDEL, MAURICE COHEN, TRACEY L COLPITTS, PAULA
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PI JU
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PI STRODE
PC C12N15/63,C12N5/10,C12Q1/68,C07K14/47//C07K16/30,G01N33/574 CC
Strandedness: Single;
CC Topology: Linear;
FH Key
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CTGAGCAGCCTGGGCATCCCCGTGAACCACCTCATAGAGGGCTCCCAGAAGTGTGTGGCT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAGCTGGGTCCCCAGGCCGTGGGGGCCCGTGAAGGCCCTGAAGGCCCTGCTGGGGGCCCTG 300
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13-NOV-2001
30-JAN-1998 JP 1998533078
31-JAN-1997 US 08/791710
PATRICIA A BILLING MEDEL, MAURICE COHEN, TRACEY L COLPITTS, PAULA
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                                                                                                                                                                                                                                                                           /organism="Zea mays"
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200 c 192 g
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| RESULT 7 AR252648 LOCUS DEFINITION ACCESSION VERSION                          | Qy<br>Db                                                    | Qу<br>Db                                                             | Qy<br>Db                                                             | Qy<br>Db                                                           | Qy<br>Db                                                           | Qy<br>Db                                                          | Query Ma<br>Best Loc<br>Matches                                                                                                                         | BASE COUNT<br>ORIGIN                                                                                   | FEATURES<br>Sour | AUTHOKS<br>TITLE<br>JOURNAL                                                                                                                                                                                                                                                                                       | SOURCE<br>ORGANISM<br>REFERENCE                  | RESULT 6 AX201348 LOCUS DEFINITION ACCESSION VERSION KEYWORDS                    | Ωy                       | Дb | Db |
|-------------------------------------------------------------------------------|-------------------------------------------------------------|----------------------------------------------------------------------|----------------------------------------------------------------------|--------------------------------------------------------------------|--------------------------------------------------------------------|-------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------|------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------|----------------------------------------------------------------------------------|--------------------------|----|----|
| AR252648 Sequence 407 from patent US 6478825. AR252648 AR252648.1 GI:27300556 | 301 ACAGTGTTTGGC 312<br>           <br>379 ACAGTGTTTGGC 390 | 241 GAGCTGGGTCCCCAGGCCGTGGGGGCCGTGAAGGCCCTGAAGGCCCTGTGGGGGGCCCTG 300 | 181 CTGAGCAGCCTGGGCATCCCCGTGAACCACCTCATAGAGGGGTCCCAGAAGTGTGTGGCT 240 | 121 GAGGCCGGGGCCGGGACCCTGGCCAACCCCTCGGCACCCTCAACCGCTGAAGCTCCTG 180 | 61 TTCTTAGTGGGCTCGGCCAAGCCTGTGGCCCAGCCTGTCGCTGCGCTGGAGTCGGCGCG 120 | 1 ATGAAGCTCGCCGCCCTCCTGGGGCTCTGCGTGGCCCTGTCCTGCAGCTCCGCTCGTGCT 60 | y Match 99.0%; Score 308.8; DB 6; Length 569;<br>Local Similarity 99.4%; Pred. No. 5.4e-39;<br>nes 310; Conservative 0; Mismatches 2; Indels 0; Gaps 0; | /organism="Homo sapiens"<br>/mol_type="genomic DNA"<br>/db_xref="taxon:9606"<br>128 a 190 c 170 g 81 t |                  | S ASIMenazi, A.J., Goddard, A., Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J., Pitti, R.M., Roy, M.A., Smith, V., Stone, D.M., Watanabe, C.K. and Wood, W.I. Compositions and methods for the treatment of tumour Patent: WO 0153486-A 27 26-JUL-2001; Patent: WO 0153486-A 27 26-JUL-2001; | Homo sapien M Homo sapien Eukaryota; Mammalia; I | AX201348  N Sequence 27 from Patent WO0153486.  AX201348  AX201348.1 GI:15391167 | 301 ACAGTGTTTGGC 312<br> |    | 02 |

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REFERENCE
AUTHORS
TITLE
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                                                                                              TITLE
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Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unclassified.

1 (bases 1 to 570)

1 (bases 1 to 570)

1 (bases 1 to 570)

Note: The implant, and Kaes, D.

Implant, method of making same and use of the implant for the treatment of bone defects

Patent: US 6478825-A 407 12-NOV-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                       AX403520 570 bp
Sequence 407 from Patent W00073454.
AX403520
                                                                                            Ashkenazi,A.J., Baker,K.P., Botstein,D., Desnoyers,L., Eaton,D., Ferrara,N., Gerber,H., Gerritsen,M., Goddard,A., Godowski,P., Grimaldi,C.J., Gurney,A.L., Kljavin,I., Napier,M.A., Pan,J., Pan,J., Fenart,T.A., Tunas,D., Watanabe,C.K., Williams,P., Wood,W.I. and Zhang,Z.
Williams,P., Wood,W.I. and Zhang,Z.
                                                                                                                                                               Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                               AX403520.1 GI:21437002
                                                                                                                                                                                                                                                                                                                              GAGCTGGGTCCCCAGGCCGTGGGGGCCCTGAAGGCCCTGAAGGCCCTGCTGGGGGCCCTG
                                                                                                                                                                                                                                                                                                                                                                   CTGAGCAGCCTGGGCATCCCCGTGAACCACCTCATAGAGGGGTCCCAGAAGTGTGTGGCT 240
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ilarity 99.4%;
Conservative
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1. 570
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190 c 170 g
                                                                           WO 0073454-A 407 07-DEC-2000;
             /organism="Homo sapiens"
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/db_xref="taxon:9606"
190 c 170 g
                                                           Location/Qualifiers
                                                                      (SD)
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pred. No. 5.4e-39;
0; Mismatches 2;
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AF313458
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SOURCE
ORGANISM
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DEFINITION
ACCESSION
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AUTHORS
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PUBMED
REFERENCE
AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 310;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                            REFERENCE
                                                                                               FEATURES
                                                                                                                                                                                                                                  JOURNAL
MEDLINE
PUBMED
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                                                                                                                                                                                                                                                                                                                                                                        AF313458
Homo sapiens UGRP2 mRNA,
AF313458
AF313458.1 GI:16565421
                                                                                                                                                                                                                                                                                                                                           Homo sapiens (human)
                                                                                                                                      3 (bases 1 to 347)
Niimi,T. and Kimura
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACACTGTTTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACAGTGTTTGGC 312
                                                                                                                                                           12438750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                        and Kimura, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99.0%;
99.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                               347 bp
complete
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UGRP1, a uteroglobin/Clara cell secretory protein-related protein, is a novel lung-enriched downstream target gene for the Typep/NKX2.1 homeodomain transcription factor Mol. Endocrinol. 15 (11), 2021-2036 (2001) 21539178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 347)

1 (bases 1, Keck-Waggoner, C.L., Popescu, N.C., Zhou, Y., Levitt, R.C., and without C.
                                                                                                                                                                                                                                                                                                        2 (bases 1 to 347)
2 (bases 1 to 347)
Niimi,T., Copeland, N.G., Gilbert,D.J., Jenkins,N.A., Srisodsai,A., Niimi,T., Copeland, N.G., Gilbert,D.J., Popescu,N.C. and Kimura,S. Zimonjic, Sexpression, and chromosomal localization of the mouse gene cloning, expression, and chromosomal localization of the mouse gene cloning, later graphs of the convel (sepb3ai, alias Ugrp2) that encodes a member of the novel (sepb3ai, alias Ugrp2) that encodes a member of the novel uteroglobin related protein gene family cytogenet. Genome Res. 97 (1-2), 120-127 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTCTTAGTGGGCTCGGCCAAGCCTGTGGCCCAGCCTGTCGCTGCGCTGGAGTCGGCGGCG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
11. .325
/codon_start=1
/product="UGRP2"
/product="HAL126217.1"
/protein_id="AAL126217.1"
/db_xref="Gi:16565422"
/translation="MKLAALLGLCVALSCSSAAAFLVGSAKPVAQPVAALESAAEAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 308.8;
Pred. No. 5.4e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4e-39
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cds.
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BASE COUNT ORIGIN

45 മ

124

O

118

g

GTLÅNPLGTLNPLKLLLSSLGIPVNHLIEGSQKCVAELGPQAVGAVKALKALLGALTV FG"

Query Match Best Local s Matches 309

Similarity

98.5%;

Conservative

309;

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Summary Statistics

Consensus quality: 124488 bases at least Q40

Consensus quality: 128031 bases at least Q30

Consensus quality: 128031 bases at least Q30

Estimated insert size: 135000; agarose-fp estimation

Estimated insert size: 135000; agarose-fp estimation

Quality coverage: 7.66 in Q20 bases; agarose-fp estimation

Quality coverage: 7.97 in Q20 bases; sum-of-contigs estimation

* NOTE: This is a 'working draft' sequence. It currently
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 GAGGCCGGGGCCGGGACCCTGGCCAACCCCTCGGCACCCTCAACCCGGTGAAGCTCCTG 180
                                                                                                                                                                                                                                                                                  Direct Submission
Direct Submission
Submitted (25-JAN-2002) Production Sequencing Facility,
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA
                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 130129)
DOE Joint Genome Institute.
Sequencing of Human Chromosome 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC108083
Homo sapiens chromosome 5 clone CTD-2013L15, WORKING SEQUENCE, 4 unordered pieces.
AC108083
AC108083.1 GI;1836929
HTG: HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAGCTGGGTCC¢CAGGCCGTGGGGGGCCGTGAAGGCCCTGAAGGCCCTGCTGGGGGGCCCTG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTGAGCAGCCTGGGCATCCCCGTGAACCACCTCATAGAGGGGTCCCAGAAGTGTGTGGCT 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTOTTAGTGGGCTCGGCCAAGCCTGTGGCCCAGCCTGTCGCTGCGCTGGAGTCGGCGGCG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATGAAGCTGGCCCCCCCTGGGGGCTCTGCGTGGCCCTGTCCTGCAGCTCCGCTGCTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATGAAGCTCGCCGCCCTCCTGGGGCTCTGCGTGGCCTGTCCTGCAGCTCCGCTCGTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 307.2; DB 9
Pred. No. 1.1e-38;
); Mismatches 3
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3 DRAFT
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94598, USA
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                                                                    REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
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TITLE
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AUTHORS
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VERSION
KEYWORDS
SOURCE
ORGANISM
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AC106813
LOCUS
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ORIGIN
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   110
Direct Submission

Submitted (12-JAN-2002) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA 3 (bases 1 to 166777)

DOE Joint Genome Institute.
                                                                                                      Sequencing of Human Unpublished
                                                                                                                        Eukaryota; Metazoa; Chordata; (Mammalla; Eutheria; Primates; (Lases 1 to 166777)
DOE Joint Genome Institute.
Sequencing of Human Chromosome
                                                                                2 (bases 1 to 166777)
DOE Joint Genome Insti
                                                                                                                                                                                                           AC106813
GI:19224876
AC106813.3 GI:19224876
HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_ACTIVEFIN.
HOMO sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               240;
                                                                                                                                                                                                                                                                              Homo sapiens chromosome 5 clone 3 ordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                        TGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         h 76.3%;
Similarity 98.8%;
40; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGAAGCTCCTGCTGAGCAGCCTGGGCATCCCCGTGAACCACCTCATAGAGGGCTCCCAGA 229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Caps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                      292
                                                                                                                                                                                                                                                                                                                                                                                                        49576
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4421
23713
23813
48603
48703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="CTD-2013L15"
/clone_lib="CalTech human
32397 c 30949 g 31146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="5"
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4420: gap of unknown length
23712: contig of 19292 bp in length
23812: gap of unknown length
48602: contig of 24790 bp in length
48702: gap of unknown length
130129: contig of 81427 bp in length
                                                                            Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 238:2;
Pred. No. 1.8e
0; Mismatches
                                                                                                                                                                   Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                 DNA
RP11-586L9,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .8e-28;
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DRAFT SEQUENCE,
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REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE

Unpublished

2 (bases 1 to 130129)
DOE Joint Genome Institute.

COMMENT

Genome Institute, 2800 Mitchell I

Project Information Center Project Name: 632820 Center clone name: CITB-H1\_2013L15

JOURNAL

ACCESSION VERSION KEYWORDS

SOURCE ORGANISM

Homo sapiens (human)

RESULT 10 AC108083 LOCUS

밁 δÃ DЬ QΥ Дb δÃ Db δÃ Дb Qγ 밁 Ş

311 301 251

ACAGTGTTTGGC

312

322

191 181

71

61 11

DEFINITION

KEYWORDS SOURCE ORGANISM

ACCESSION VERSION LOCUS DEFINITION

REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS

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COMMENT
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JOURNAL
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RESULT 12
AC025336/c
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Best Local
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Consensus quality: 166071 bases at least Q40

Consensus quality: 166072 bases at least Q20

Consensus quality: 166325 bases at least Q20

Consensus quality: 166325 bases at least Q20

Consensus quality: 166377; sum-of-contigs estimation

Estimated insert size: 166577; sum-of-contigs estimation

Quality coverage: 9.4 in Q20 bases; sum-of-contigs estimation

Quality coverage: 10.51 in Q20 bases; sum-of-contigs estimation

Quality coverage: 3 contigs draft' sequence. It currently

* NOTE: This is a 'working draft' sequence. It currently

* consists of 3 contigs days between the contigs

* are represented as runs of N. The order of the pieces

* are represented as runs of N. The order of the pieces

* are the gaps between them are based on estimates that have

* of the gaps between them are based on estimates that have

* of the gaps between them are based on estimates that have

* provided by the submittor.

* the accession number will be replaced

* the accession number will be preserved.

* the accession number will be preserved.

* the accession provided by the submittor of 62237 bp in length

* 62338 62337: gap of unknown length

* 75838 6237: contig of 62237 bp in length

* 75838 16777: contig of 13500 bp in length

* 75838 16777: contig of 90840 bp in length

* 75838 166777

Ource Consense Homo Saplens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center: Joint Genome Institute Center Code: JGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Project Information
Center Project Name: 1519801
Center clone name: RPCI-11_586L9
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/Clone_lib="RPCI human BAC library 200 others
39804 c 41258 g 40888 t 200 others
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98.8%;
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RS Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,

RS Birren, B., Linton, L., Barna, N., Bastien, V., Beda, F.,

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Pisani, C., Pollara, V., Norman, C.H., McCarre, N., McCarre, N.,

Norman, C., Land, 
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AC025336 GI:7328761 AC025336.2 GI:7328761
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1 (bases 1 to 168347)

1 Linton, L., Nusbaum, C. and Lander, E.

Homo saplens chromosome 5, clone RP11-451H23

Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NOTE: This is a 'working draft' sequence. It currently consists of 32 contigs. The true order of the pleces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Insert size: 165247; sum-of-contigs onality coverage: 3.6 in Q20 bases; sum-of-contigs
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1490
3131
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1389: contig of 1389 bp in length
1489: gap of 100 bp
1319: contig of 1641 bp in length
3230: gap of 100 bp
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COMMENT

g of 1712 bp : f 100 bp g of 1939 bp : 100 bp g of 1627 bp 100 bp of 1478 bp in 100 bp

in in in length

length length

ig of 1826 bp in length
of 100 bp
ig of 2346 bp in length
of 100 bp
of 3183 bp in length
of 100 bp
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of 3556 bp in length
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| 230 AGTGTGTG | 143927 TGAAGCTC                                                                                             |          | 144047 CAGCTGCC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | Ouery Match Best Local Similarity 98.8%; Matches 240; Conservative 50 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC         | c_feature                              | misc_feature              |                                           | <pre>misc_feature misc_feature</pre> | misc_feature                                        | misc_feature                                                | misc_feature                              | misc_feature                             | misc_feature                            | misc_feature                            | misc_feature                            | misc_feature                            | misc_feature                            | misc_feature                            | misc_feature                         | misc_feature                            | misc_feature                                    | misc_feature                            | misc_feature                            | misc_feature                            | misc_feature                            | misc_feature                               | misc_feature                            | misc_feature                           | misc_feature                          | misc_feature                       |
| 289          | TVAAVGUUCUTGCTGAGCAGCACCTGGGCATCCCCGTGAACCACCTCATAGAGGGCTCCCAGA 229 TIHIHITIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIH |          | The first of the control of the co | 76.3%; Score 238.2; DB 2; Length 168347; lty 98.8%; Pred. No. 1.7e-28; ervative 0; Mismatches 3; Indels 0; Gaps 0; | /note="assembly_fragment" 130569142239 | /note="assembly_fragment" | /note="assembly_fragment"<br>108116118144 | 9015499426                           | /note="assembly_fragment" /note="assembly fragment" | /note="assembly_fragment"<br>7667983312<br>/note="security" | /note="assembly_fragment"<br>71669. 76578 | /note="assembly_fragment"<br>66825 71568 | /note="assembly_fragment"<br>6165866724 | /note="assembly_fragment"<br>5668861557 | /note="assembly_fragment"<br>5268756567 | /note="assembly_fragment"<br>4791752586 | /note="assembly_fragment"<br>4240347816 | /note="assembly_fragment"<br>3737842302 | /note="assembly_fragment" 3381537277 | /note="assembly_fragment"<br>3128933714 | <pre>/note="assembly_fragment" 2786931188</pre> | /note="assembly_fragment"<br>2509327768 | /note="assembly_fragment"<br>2139824992 | /note="assembly_fragment"<br>1804221297 | /note="assembly_fragment"<br>1475917941 | /note="assembly_fragment"<br>12313.".14658 | /note="assembly_fragment"<br>1038712212 | /note="assembly_fragment"<br>889910286 | /note="assembly_fragment"<br>70828708 | /note="assembly_fragment" 50436981 |

31188 31188 3218 bp in length 3320 bp in length 3328 33714; contig of 3425 bp in length 33218 33714; contig of 3425 bp in length 33718 33714; contig of 3425 bp in length 33718 33717; contig of 3425 bp in length 37378 33717; contig of 343 bp in length 47317 42402; apap of 100 bp 42403 42402; apap of 100 bp 56568 56667; contig of 3881 bp in length 52586; contig of 4670 bp in length 52586; contig of 584 bp in length 56568 61557; contig of 586 bp in length 66725 66824; contig of 586 bp in length 66825 66824; contig of 586 bp in length 71569 71568; contig of 4890 bp in length 76579 76578; contig of 4890 bp in length 916825; contig of 586 bp in length 916824; contig of 586 bp in length 916825; contig of 586 bp in length 916826; contig of 587 bp in length 916824; contig of 588 bp in length 916824; contig of 588 bp in

FEATURES source

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                                                                                                                                                                                                            240;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 www-shgc.stanford.edu
qww-shgc.stanford.edu
quality: Phrap Quality >=40 99.8% of Sequence;
Estimated Total Number of Errors is 0.9.
ROTE: Shatter libraries failed to verify the dinucleotide repeat
region 124370-125308. Unsure number of repeat copies
124370-125308. Forced join 124996.
Location/Qualifiers
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Submitted (25-MAY-2002) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USS 3 (bases 1 to 19024)

DOE Joint Genome Institute and Stanford Human Genome Center.

Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (04-MAR-2003) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Mar 4, 2003 this sequence version replaced gi:21206277. Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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DOE Joint Genome Institute and Stanford Human Genome Center.
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                           TGAAGCTCCTGCTGAGCAGCCTGGGCATCCCCGTGAACCACCTCATAGAGGGCTCCCAGA
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Summary Statistics

Consensus quality: 110477 bases at least Q40

Consensus quality: 117221 bases at least Q30

Consensus quality: 120225 bases at least Q20

Estimated insert size: 131000; pulse field gel estimation

Estimated insert size: 126288; sum-of-contigs estimation

Quality coverage: 7.48 in Q20 bases; pulse field gel estimation

Quality coverage: 7.76 in Q20 bases; sum-of-contigs estimation.

* NOTE: This is a 'working draft' sequence. It currently

* consists of 13 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
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Center Project Name: 78060
Center Project Name: CIT978SKB_36B8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 127488)
DOE Joint Genome Institute.
Sequencing of Human Chromosome 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 (bases 1 to 127488)
DOE Joint Genome Institute.
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HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN
                                    5006
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ne 5 clone CTB-36B8, WORKING
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of 3395
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of 2103
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of 2490
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of 2542
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of 1493
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of 1038 bp in length
unknown length
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of 8361
unknown
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SEQUENCE,
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RESULT 15
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ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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Zea mays

Elkaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

Clade; Panicoideae; Andropogoneae; Zea

Clade; Panicoideae; Andropogoneae; Zea

El (bases 1 to 25)

KS Medel, P.A.B., Cohen,M., Colpitts,T.L., Friedman,P.N., Gordon,J.,

Rodens, S.C., Klass,M.R., Kratochvil,J.D., Rapp,L.R.,

Russell,J.C. and Stroupe,S.D.

Reagents and methods useful for detecting diseases of the lung

Patent: JP 2001522225-A 3 13-NOV-2001;

ABBOTT LABORATORIES

PN JP 2001522225-A,3

PP 31-JAN-1998 JP 1998533078

PF 31-JAN-1997 US 08/791710

PI PATRICIA A BILLING MEDEL, MAURICE COHEN, TRACEY L COLPITTS, PAULA
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240; Conservative
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JP 2001522225-A/3.
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JON D KRATOCHVIL, LISA ROBERTS RAPP, JOHN C RUSSELL, STEPHEN D
                              JULIAN GORDON, EDWARD N GRANADOS, STEVEN C HODGES, MICHAEL R PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24497
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1. 127488
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/mol_type="genomic DNA"
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/clone_lib="CalTech human BAC library B"
32392 c 31616 g 30626 t 1211 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39085: contig of 14589 bp in length
39185: gap of unknown length
60545: contig of 21360 bp in length
60645: gap of unknown length
79490: contig of 18845 bp in length
79590: gap of unknown length
79590: gap of unknown length
127488: contig of 47898 bp in length.
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                                                                                                                                                                                                                                                                                                                                                                                                     linear PAT 27-AUG-2002 diseases of the lung.
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Matches 183;
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                                         181 GGC
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                                                                                                      190 CTGGGCATCCCCGTGAACCACCTCATAGAGGGCTCCCAGAAGTGTGTGGGTGAGCTGGGT 249
                                                                                       61 CTGGGCATCCCCGTGAACCACCTCATAGAGGGCTCCCAGAAGTGTGTGGGCTGAGCTGGGT
                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                          C C12N15/63,C12N5/10,C12Q1/68,C07K14/47//C07K16/30,G01N33/574 CC
Strandedness: Single;
C Topology: Linear;
H Key C Location/Qualifiers.
                                                                                                                                                                               58.7%; Score 183; I ilarity 100.0%; Pred. No. 2. Conservative 0; Mismatches
                                                                                                                                                                                                                                     /organism="zea mays"
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76 c 74 g
                                                                                                                                                                                                                                                                                   Location/Qualifiers.
Location/Qualifiers
1...225
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2.6e-19;
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Search completed: September 20, 2003, 00:34:59 Job time: 1404.59 secs

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Title:
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Sequence:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           September 19, 2003, 23:17:58; Search time 2466.41 Seconds (without alignments) 9139.272 Million cell updates/sec
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2: gb_htg:
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gb_htg:*
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gb_ov:*
gb_ov:*
gb_pat:*
gb_ph:*
em_htg_hum:*
em_htg_inv:*
em_htg_other:*
em_htg_other:*
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Pred. No.

İS

the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| REFERENCE<br>AUTHORS<br>TITLE                                        | VERSION KEYWORDS SOURCE ORGANISM           | RESULT 1 AC022095/c LOCUS DEFINITION                          | •          | C 44<br>45                               | 4 4 2<br>4 3 2 F                       | 4 4<br>0 4<br>0 6 | c 37                 |         | 0 0<br>2 2 2<br>2 4 7 |                     |                      | c 28     | c 26<br>27           | 25       |                                          | 222                                      | 19                                       |                      | c 16     |                     |                    | 11                | 1 9      | 8                 | וסנ      | л 4-               | ω c      | ) <del> </del>     | Sult<br>No. |
|----------------------------------------------------------------------|--------------------------------------------|---------------------------------------------------------------|------------|------------------------------------------|----------------------------------------|-------------------|----------------------|---------|-----------------------|---------------------|----------------------|----------|----------------------|----------|------------------------------------------|------------------------------------------|------------------------------------------|----------------------|----------|---------------------|--------------------|-------------------|----------|-------------------|----------|--------------------|----------|--------------------|-------------|
| S D 1 M                                                              | ####                                       | 1. H. A.                                                      |            | ω ω                                      | 55 55 55 55 55 55 55 55 55 55 55 55 55 | 0.00.0            |                      | ω,      | л.                    | ٥٥.                 | > ⊢                  |          |                      |          | 61.8                                     | 7 10 0                                   | uω                                       | 4 4                  | 50.0     | ٠,                  | 77                 | 78                | 78       | <b>7</b> –        | 120      | J .                | 48       | ٠.                 | Score       |
| Eukaryota;<br>Mammalia; I<br>1 (bases :<br>DOE Joint (<br>Sequencing | TG; HTGS_PHA<br>DMO sapiens<br>DMO sapiens | )22095<br>no sapi<br>unorde                                   |            | 0.                                       | 10.6                                   | 000               | 000                  | 0:      | 00:                   | 011                 | ٠,                   | 11.2     |                      | Η!       | 111.2                                    | - <u></u> -                              |                                          | 11.8<br>11.7         |          |                     | ω.                 | 14.2              | - +-     |                   |          | , 01               | ω.       | υ                  | Query       |
| Meta                                                                 | St                                         | ъc                                                            |            | NN                                       |                                        |                   | Ν                    |         | Ŋ                     | μ.                  | ٠.                   | μH       | Н.                   |          | <u> </u>                                 | ٠,                                       |                                          | 63082<br>991         | 219952   | 172650              | K 1                | 570               | 569      | 519               | 562      | 130129             | 190024   | n Ńo               | Length      |
| a;<br>a;<br>748<br>Ins                                               | 699<br>H1                                  | 1<br>hromosome<br>ieces.                                      |            |                                          | യത                                     |                   | ) N N                | ヒ       | 19                    | 11                  | o o                  | N        | φΝ                   | 10       | 225                                      | 126                                      | 21                                       | 11                   | 2 1      | 2                   | 90                 | 000               | ע ע      | თ თ               | 9        | งผ                 | 9 4      | N C                | DB          |
| hordata; Cran<br>rimates; Cata<br>)<br>itute.<br>hromosome 5         | 18<br>S_DRAFT; HTGS.                       | 27488 bp<br>5 clone CTE                                       | ALIGNMENTS |                                          | AX411<br>HSGG1                         |                   | ACU66610<br>AC138109 | PM2A12B | AC011407<br>PM7G11B   | AP005743<br>PM2B12B | AC112672<br>AC141419 | AC091093 | AC139773<br>AF429315 | AF411253 | AC141871                                 | AC022663                                 | PM3H11G                                  | AC022663<br>PM12H12B | AC084804 | AP005772            | AF429315           | AX403520          | AX201348 | BD082142          | BD082141 | AC108083           | AC122714 | AC022095           | ID          |
| iata; Vertebrata; Euteleostomi;<br>rrhini; Hominidae; Homo.          | _ACTIVEFIN.                                | DNA linear HTG 20-APR-2001<br>B-36B8, WORKING DRAFT SEQUENCE, |            | AC134836 Mus muscu<br>AE006462 Homo sapi | DNA                                    | Sequ              |                      |         | Hom                   |                     | Mus                  | Pap      | AF429315 Homo sapi   | Mus      | AC027353 Homo sapi<br>AC141871 Mus muscu | AC022663 Homo sapi<br>AL684839 Penicilli | AL685749 Penicilli<br>AC143286 Macaca mu | Penicill             | Mus      | Oryza sa<br>Penicil | AF429315 Homo sapi | AX403520 Sequence | ຜູ້ຜູ    | BD082142 Reagents | Reagents | AC108083 Homo sapi | domo sap | ACO22095 Homo sapi | Description |

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REFERENCE
AUTHORS
TITLE
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                                                                               Query Match 88.7%;
Best Local Similarity 95.8%;
Matches 529; Conservative
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Consensus quality: 110477 bases at least Q40

Consensus quality: 117221 bases at least Q30

Consensus quality: 120225 bases at least Q30

Consensus quality: 120225 bases at least Q30

Estimated insert size: 131000; pulse field gel estimation

Estimated insert size: 126288; sum-of-contigs estimation

Quality coverage: 7.48 in Q20 bases; pulse field gel estimation

Voulity coverage: 7.76 in Q20 bases; sum-of-contigs estimation.

* NOTE: This is a 'working draft' sequence. It currently

* consists of 113 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
1 CGGCCGGGGAGGCGGGAGTGAGGCCTGATCGTCCCTGGCGCCTCCACCTCCCCAGG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             unpublished
2 (bases 1 to 127488)
2 (bases 1 to 127488)
2 (chases 1 to 127488)
5 (chases 1 to 127488)
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Center Project Name: 78060
Center clone name: CIT978SKB_36B8
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32392 c 31616 g 30626 t 1211 others
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1216: gap of unknown length
1224: contig of 1038 bp in length
2354: gap of unknown length
3412: contig of 1058 bp in length
3512: gap of unknown length
5005: contig of 1493 bp in length
5105: gap of unknown length
7647: contig of 5442 bp in length
7747: gap of unknown length
10237: contig of 2490 bp in length
10337: gap of unknown length
10338: contig of 2490 bp in length
10400: contig of 3395 bp in length
15933: contig of 3395 bp in length
15933: contig of 3395 bp in length
16033: gap of unknown length
16033: gap of unknown length
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7. gap of unknown length
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0. gap of unknown length
5. contig of 3395 bp in length
6. contig of 8361 bp in length
6. contig of 8361 bp in length
6. contig of 14589 bp in length
5. contig of 14589 bp in length
5. contig of 21360 bp in length
5. gap of unknown length
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6. gap of unknown length
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                                                                                         0;
                                                                                    Score 488.6; DB 2;
Pred. No. 1.4e-72;
D; Mismatches 5;
                                                                                    Indels 18; Gaps
                                                                                                                                                                              Length 127488;
                                                                                    2
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| RESULT 2 ACC02536/G LOCUS DEFINITION ACCESSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | Qy<br>Db 83                                                 | Qy<br>Db 83                                                          | QY<br>Db 83                                                              | Qy<br>Db 83                                                             | Qy<br>Db 84                                                              | Qy<br>Db 84                                                              | Qy<br>Db 84                                             | Qy<br>Db 84                                 | Qy<br>Db 84                                                         | Db 84 |
|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------|----------------------------------------------------------------------|--------------------------------------------------------------------------|-------------------------------------------------------------------------|--------------------------------------------------------------------------|--------------------------------------------------------------------------|---------------------------------------------------------|---------------------------------------------|---------------------------------------------------------------------|-------|
| AC025336 Homo sapiens chromosome 5 clone RP11-451H23 map 5, WORKING DRAFT SEQUENCE, 32 unordered pieces. AC025336 AC025336 AC025336 AC025336 AC025336 AC025336 AC025336 AC025336 AC025336 AC025336 AC025336 AC025336 AC025336 AC025336 AC025336 AC025336 AC025336 AC025336 AC025336 AC025336 AC025336 AC025336 AC025336 AC025336 AC025336 AC025336 AC025336 AC025336 AC025336 AC025336 AC025366 AC025336 AC02536 AC025336 AC02536 AC025336 AC025336 AC02536 AC02536 AC02536 AC02536 AC02536 AC025336 AC02536 | 540 AGCCCCCGCGCC 551<br>          <br>768 AGCCCCGCGCC 83757 | 480 ACCGGGTATAAGAAGCCTCGTGGCCTTGCCCGGGCAGCCGCAGGTTCCCCGCGCGCCCCC 539 | 420 GAGCGGAGCGGGCAGGGCTTTCTCAGGAGCGCGGGCGAGGCCGGCGGCGCGGGGGGAGGCGAGG 479 | 360 GGGGCACGGGCTTCCCAGGGCCCGCCGCCGCAGCAGGAAGTTGGCCAGGGCACGGCCGT 419<br> | 301 CT-CTCTCAGAGGGCCCCAGCGCCTGCCAAGAGGAAGTCCTCGAGGCCCGGGCAGGGAAG 359<br> | 241 AGACCGCAAAGCGAAGGTGCGGGCCGGGGTGGGCCTCGCGGAGACAAAGGCCGGGCCTGC 300<br> | 181 CCCTCACCNGAGGGAAGCTCCCCTCACCCGGCCCAGCCCTGCAGGGGGGGG | 121 CAGGGACCAGGGAGCCAGGAACTGCGCCGCCCCCCCCCC | 61 CGCAGAAGGCGCCCACGAGGACCCCCAGTGCCCGACGTTGCCACGGTCTGGGATCAGAGG 120 |       |

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COMMENT
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Submitted (08-MAR-2000) Whitehead Institute/MIT Center for Genome Submitted (08-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA no Mar 25, 2000 this sequence version replaced gi:/210017.

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html

http://ftp.genome.washington.edu/RM/RepeatMasker.html

center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Vassiltev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center project name: L6686

Center clone name: L6686

Center clone name: 451,H,23

Sequencing vector: M13; M77815; 100% of reads
Sequencing vector: M13; M77815; 100% of reads
Sequencing vector: Phrap; version 0.960731

Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731

Consensus quality: 150422 bases at least Q40
Consensus quality: 159524 bases at least Q30
Consensus quality: 159524 bases at least Q20
Insert size: 156347; sum-of-contigs
Quality coverage: 3.6 in Q20 bases; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
                                                                  31289
33715
33815
37278
37378
42303
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31189
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1: contig of 385 bp in length
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f 100 bp in 1
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of 4670
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61558 666724: contig of 4890 bp in 16
61558 66724: contig of 4890 bp in 16
61572 66824: gap of 100 bp
6825 71568: contig of 5067 bp in 1en
569 71568: gap of 100 bp
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79 83312: contig of 634 bp in 1engt
79 83312: gap of 100 bp
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528; Conserv
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Pred. No. 3.6e-72;
0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 168347;
               linear
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inear PRI 04-MAR-2003 complete sequence.
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AUTHORS
TITLE
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AUTHORS
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AUTHORS
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VERSION
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Matches 528;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AL Submitted (25-MAY-2002) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA Direct Submission

AL Submitted (04-MAR-2003) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Mar 4, 2003 this sequence version replaced gi:21206277. Draft Sequence Produced by DOE Joint Genome Institute Finishing Completed at Stanford Human Genome Center www-shgc.stanford.edu Quality: Phrap Quality >=40 99.8% of Sequence; Shatter libraries failed to verify the dinucleotide repeat region 124370-125308. Unsure number of repeat copies Location/Qualifiers

1 19024
                                                                                                                                                                      81351
                                                                                                                    81291
                                                                                                                                                                                                                    301 CT-CTCTCAGAGGGCCCCAGCGCCTGCCAAGAGGAAGTCCTCGAGGCCCGGGCAGGGAAG
                                                                                         241
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AC122714.2
HTG.
                                                                                                                                                                                                                                                                                                                                                Similarity
 CTGCTCTCAGAGGGCCCCAGCGCCTGCCAAGAGGAAGTCCTCGAGGCCCGGGGCAGGGAAG
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                                                                                                          2 (bases 1 to 190024)
DOE Joint Genome Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleos Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 190024) DOE Joint Genome Institute and Stanford Human Genome Center. Direct Submission
                                                      AGACCGCAAAGCGAAGGTGCGGGCCGGGGTGGGCCTCGCGGAGACAAAGGCCGGGCCTGC
                                                                      AGACCGCAAAGCGAAGGTGCGGGCCGGGGTGGGCCTCGCGGAGACAAAGGCCGGGGCCTGC
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                                                                                                                                                                                                                                                                                                                                                                                         /note="NOTE: Shatter libraries failed to verify the dinucleotide repeat region 124370-125308. Unsure number of repeat copies 124370-125308. Forced join 124996." a 46028 c 46121 g 52268 t
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95.7%;
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                                                                                                                                                                                                                                                                                                                             Score 486; DB 9; I
Pred. No. 3.4e-72;
D; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                        Length 190024;
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Query Match Best Local

misc\_feature

misc\_feature misc\_feature

misc\_feature misc\_feature

misc\_feature

misc\_feature misc\_feature misc\_feature

misc\_feature

RESULT 3
AC122714/c
LOCUS
DEFINITION

Homo

B VΩ В Q В QΥ 밁 γ ₽ QY В Qy В δÃ ₽ Qγ В QΥ В δÃ

144920

301

360

145022

181

145082

145142

61

δÃ

QΥ

Qy g VQ Вþ

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RESULT 4
AC108083/c
LOCUS
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AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
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VERSION
KEYWORDS
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                          FEATURES
              source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81129
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Consensus quality: 128042 bases at least Q30
Consensus quality: 128042 bases at least Q30
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Estimated insert size: 129829; sum-of-contigs estimation
Quality coverage: 7.66 in Q20 bases; agarose-fp estimation
Quality coverage: 7.97 in Q20 bases; sum-of-contigs estimation.

* NOTE: This is a 'working draft' sequence. It currently

* NOTE: This is a 'working draft' sequence record is

* consists of 4 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* arbitrary. Gaps between the stages of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (25-JAN-2002) Production Sequencing
Genome Institute, 2800 Mitchell Drive, Walnut
-------Genome Center
Center: Joint Genome Institute
Center: Code: JGI Transital documents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
Eukaryota; Metazoa; Chordata; (
Mammalia; Eutheria; Primates; (
1 (bases 1 to 130129)
DOE Joint Genome Institute.
Sequencing of Human Chromosome
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AC108083.1 GI:18369929
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Center Project Name: 632820
Center clone name: CITB-H1_2013L15
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g Joint Genome Institute.
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23713
23813
23813
48603
48703
/organism="Homo
                             Location/
                        4320: contig of 4320 bp in length
4420: gap of unknown length
23712: contig of 19292 bp in length
23812: gap of unknown length
48602: contig of 24790 bp in length
48702: gap of unknown length
130129: contig of 81427 bp in length.
coation/qualifiers
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Creek, CA
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Matches 522; Conserv
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                                                      Eukaryota; Motazoa; Chordata; Ci
Mammalia; Eutheria; Primates; Ca
1 (bases 1 to 166777)
DoE Joint Genome Institute.
Sequencing of Human Chromosome 5
Unpublished
2 (bases 1 to 166777)
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              Direct Submission Submitted (12-JAN-2002) Production
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                                           DOE
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                                        (bases 1 to 166777)
3 Joint Genome Institute
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AC106813

Homo sapiens chromosome 5 clone 3 ordered pieces.
AC106813

AC106813 GI:19224876

HTGS_PHASE2; HTGS_DRAFT; HT
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/db_xref="taxon:9606"
/chonosome="5"
/clone="0TD-2013L15"
/clone="iD="CalTech human B
/clone_lib="CalTech human B
/ 32397 c 30949 g 31146 t
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DRAFT SEQUENCE,
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Craniata; Vertebrata; Catarrhini; Hominidae;

Euteleostomí; Homo.

Sequencing

facility,

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Best Local
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Matches 528; Conserv
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                                                                                                                                                                                                                                                 61 CGCAGAAGGCGĆCCACGAGGACCCCCAGTGCCCGACGTTGCCACGGTCTGGGATCAGAGG
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Consensus quality: 166432 bases at least Q30
Consensus quality: 166432 bases at least Q30
Consensus quality: 166432 bases at least Q30
Estimated insert size: 186250; agarose-fp estimation
Estimated insert size: 186250; agarose-fp estimation
Quality coverage: 9.4 in Q20 bases; agarose-fp estimation
Quality coverage: 10.51 in Q20 bases; sum-of-contigs estimation
Quality coverage: 10.51 in Q20 bases; sum-of-contigs
* NOTE: This, is a 'working draft' sequence. It currently
* consists of 3 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.

* This sequence will be replaced
* the accession number will be preserved.

* the accession number will be preserved.

* 62238 | 62337: gap of unknown length
* 6238 | 75937: gap of unknown length
* 75938 | 166777: contig of 13500 bp in length
* 75938 | 166777: contig of 90840 bp in length.
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Center Project Name: 1519801
Center clone name: RPCI-11_586L9
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Center Code: JGI
Web site: http://www.jgi.doe.gov
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Submitted (07-MAR-2002) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Mar 7, 2002 this sequence version replaced gi:18369924.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Summary Statistics
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DOE Joint Genome Institute.
                                            AGACCGCAAAGCGAAGGTGCGGGCCGGGGTGGGCCTCGCGGAGACAAAGGCCGGGCCTGC
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/clone_lib="RPCI human BAC library
39804 c 41258 g 40888 t 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="5"
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to 166777)
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Pred. No. 2.4e-70;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Medel, P.A.B., Cohen, M., Colpitts, T.L., Friedman, P.N., Gordon, J. Granados, E.N., Hodges, S.C., Klass, M.R., Kratochvil, J.D., Rapp, I. Russell, J.C. and Stroupe, S.D.
Reagents and methods useful for detecting diseases of the lung Patent: JP 200152225-A 5 13-NOV-2001;
ABBOTT LABORATORIES PN JP 200152225-A/5
DD 13-NOV-2001
DT 30-JAN-1997 US 08,791710
PATRICIA A BILLING MEDEL, MAURICE COHEN, TRACEY L COLPITTS, P
                                                                                                                                                                                                                                                                                                                                                                                                   P. P. I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 562)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      KLASS
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C12N15/63,C12N5/10,C12Q1/68,C07K14/47//C07K16/30,G01N33/574 CC
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Key
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                                                                                                                                                                                                                                                                                                                                                                                                                              JON D KRATOCHVIL, LISA ROBERTS RAPP, JOHN C RUSSELL, STEPHEN D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PATRICIA A BILLING MEDEL, MAURICE COHEN, TRACEY L COLPITTS, PAULA
                                                                                                                                                                                                                        /organism="Zea mays"
/mol_type="genomic DNA"
/db_xref="taxon:4577"
200 c 192 g
                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GORDON, EDWARD N GRANADOS, STEVEN C HODGES, MICHAEL R
                                                                                                                                                     21.8%;
                                                                                                                                                                                                                                                                                                                                                                           Single;
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                                                                                                                                Score 120; DB 6;
Pred. No. 1.4e-10;
0; Mismatches 1
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                                                                                                                                                                    Length 562
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Gordon, J. Rapp, L.R.,

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RESULT 7
BD082137
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JOURNAL
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Best Local Similarity 96.7
Matches 117; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              source
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2E 1 (bases 1 to 190)
RS Medel, P. A. B., Cohen, M., Colpitts, T. L., Friedman, P. N., Gordon, J., Rodges, S. C., Klass, M. R., Kratochvil, J. D., Rapp, L. R., Russell, J. C. and Stroupe, S. D. Rasgents and methods useful for detecting diseases of the lung Patent: JP 200152225-A 1 13-NOV-2001; ABBOTT LABORATORIES
PN JP 200152225-A/1
PD 13-NOV-2001
PD 30-AN-1998 JP 198533078
PR 31-AN-1998 JP 198533078
PR 31-AN-1998 JP 198533078
PR 31-AN-1998 JP 198533078
PR 31-AN-1997 US 08/791710
PI PATRICIA A BILLING MEDEL, MAURICE COHEN, TRACEY L COLPITTS, PAULA
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Reagents and methods useful f
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JP 2001522225-A/1.
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BD082142 519
Reagents and methods useful
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JP 2001522225-A/6.
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C12N15/63, C12N5/10, C12Q1/68, C07K14/47//C07K16/30, G01N33/574 CC
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JULIAN GORDON, EDWARD N GRANADOS, STEVEN C HODGES, MICHAEL R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Topology: Linear;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Zea mays"
/mol_type="genomic DNA"
/db_xref="taxon:4577"
69 c 67 g
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Location/Qualifiers
1...190
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detecting diseases
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JOURNAL
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CC
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Sequence 27 from Patent W00153486.
AX201348 ------
                                                                                                                                                                           Ashkenazi,A.J., Goddard,A., Godowski,P.J., Gurney,A.L., Hillan,K.J., Marsters,S.A., Pan,J., Pitti,R.M., Roy,M.A., Stone,D.M., Watanabe,C.K. and Wood,W.I. Compositions and methods for the treatment of tumour Patent: WO 0153486-A 27 26-JUL-2001;
                                                                                                                                                                                                                                                                                                                                               Homo sapiens (human)
                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Strandedness: Single;
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                                                                                                                                                            Genentech,
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                                    128
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/mol_type="genomic DNA"
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190 c 170 g
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1. .519
                                    /organism="Homo sapiens"
/mol_type="genomic DNA"
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190 c 170 g 8
                                                                                                                       Location/Qualifiers
1. .569
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FEATURES
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AUTHORS
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SOURCE
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FEATURES
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AX403520
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AUTHORS
TITLE
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AR252648
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Best Local S
Matches 78
                                                                                                      TITLE
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Best Local Similarity
Matches 78; Conserv
                                    source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unknown.
Unclassified.
1 (bases 1 to 570)
1 (bases 1 to 570)
1 (bases 1 to 570)
2 Minterbottom, J.M., Shimp, L., Boyce, T.M. and Kaes, D.
2 Implant, method of making same and use of the implant for the treatment of bone defects
2 Patent: US 6478825-A 407 12-NOV-2002;
2 Location/Qualifiers
3 1. 570 ---"nnknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      474 GCGAGGACCGGGTATAAGAAGCCTCGTGGCCTTGCCCGGGGCAGCCGCAGCTTCCCCGCGC
                                                                                                            Ashkenazi, A.J., Baker, K.P., Botstein, D., Desnoyers, L., Eaton, D., Ferrara, N., Gerber, H., Gerritsen, M., Goddard, A., Godowski, P., Grimaldi, C.J., [Gurney, A.L., Kljavin, I., Napier, M.A., Pan, J., Paoni, N.F., Roy, M., Stewart, T.A., Tumas, D., Watanabe, C.K., Williams, P., Wood, W.I. and Zhang, Z.
                                                                                                                                                                                      Homo sapiens (human)
Homo sapiens (human)
Eukaryota; Metizoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                            Genentech
                                                                                            Secreted and transmembrane polypeptides and nucleic acids encoding
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Sequence 407 from Patent
AX403520
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78; Conservative
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ilarity | 100.0%; Pred. No. 0.0014;
Conservative 0; Mismatches 0;
                                           WO 0073454-A 407 07-DEC-2000;
ch Inc. (US)
Location/Qualifiers
    /organism="Homo sapiens"
/mol_type="genomic DNA"
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100.0%; Pred. No.
Live 0; Mismatc
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Best Local
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                                                                                                                                                                                                                                                                      source
                                    61
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Ъ Qy В VΩ

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD: Clade; Panicodeae; Andropogoneae; Zea.

E 1 (bases 1 to 244)

KS Medel, P.A.B., Cohen, M., Colpitts, T.L., Friedman, P.N., Gordon, J., Granados, E.N., Hodges, S.C., Klass, M.R., Kratochvil, J.D., Rapp, L.R., Russell, J.C. and Stroupe, S.D.

Reagents and methods useful for detecting diseases of the lung absort LABORATORIES
PN JP 200152225-A 2 13-NOV-2001;
PD J-200152225-A 2 13-NOV-2001;
PD J-200152225-A 2 13-NOV-2001;
PP 31-JAN-1997 US 08/791710
PI PATRICIA A BILLING MEDEL, MAURICE COHEN, TRACEY L COLPITTS, PAULA
                                                   474 GCGAGGACCGGGTATAAGAAGCCTCGTGGCCTTGCCCGGGCAGGCTGCCGCGCGC 533
                           534 GCCCCGAGCCCCGCGCC 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  534 GCCCGAGCCCCGCGCC 551
||||||||||||||||||||||||||||||||||61 GCCCGAGCCCCCGCGCC 78
                                                                                                                                                                                                                                                                                                                                         PI N
RLASS,
PI JO
PI SI
PC CI
                                                                                                                                                                                                                                                                                                 Strandedness:
CC Topology:
FH Key
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Reagents and methods useful 1
BD082138
BD082138.1 GI:22627748
JP 2001522225-A/2.
                                                                                                                                        Similarity
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1 Similarity 100.0%;
78; Conservative
GCCCCGAGCCCCCGCGCC
                                                                                                                                                                                                       25
                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                               Topology: Linear;
Key
                                                                                                                                                                                                                                                                                                                   C12N15/63,C12N5/10,C12Q1/68,C07K14/47//C07K16/30,G01N33/574 CC
                                                                                                                                                                                                                                                                                                                                                            JON D KRATOCHVIL, LISA ROBERTS RAPP, JOHN C RUSSELL, STEPHEN D
                                                                                                                                                                                                                                                                                                                                                                                                 N FRIEDMAN,
JULIAN GORDON, EDWARD N GRANADOS, STEVEN C HODGES, MICHAEL R
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                                                                                                                                                                                               /organism="Zea mays"
/mol_type="genomic DNA"
/db_xref="taxon:4577"
97 c 82 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:9606"
a 190 c 170 g
                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                  14.0%;
98.7%;
78
                                                                                                                     Score 77; DB
Pred. No. 0.00
0; Mismatches
                                                                                                                         0,
                                                                                                                                                                                                                                                                                             ocation/Qualifiers
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                                                                                                                DB 6;
0.0026;
1;
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0.0014;
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 64; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL
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                                                                                                                                                                                                                                                                                       17694 SSTSYSYSCCWKMSSWGSCYKCMKYYSGWSSYSTSMGYYSSTSCKKYKCSWSSMYKCKTS 17635
                                                                                                                                                                     17634 KSYRRKRSYYWGGGKRAKKKYYCAGRRRRMSYWKCCAKWWMSYCCWSYCMTYYYSKSCT 17575
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Homo sapiens junctophilin 3 (
AF429315
AF429315.1 GI:17646244
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1 (bases 1 to 125020)

Holmes, S. E., O'Hearn, E., Rosenblatt, A., Callahan, C., Hwang, H.S., Ingersoll-Ashworth, R.G., Fleisher, A., Stevanin, G., Brice, A., Potter, N.T., Ross, C.A. and Margolis, R.L.

A repeat expansion in the gene encoding junctophilin-3 is associated with Huntington disease-like 2

Nat. Genet. 29 (4), 377-378 (2001)
                                                                                                                                                                                                                                                                                                                                          45 CCTCCACCTCCCCAGGCGCAGAAGGCGCCCACGAGGACCCCCAGTGCCCGACGTTGCCAC
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Holmes, S.E., Ingersoll-Ashworth, R.G., Ross
Direct Submission
Submitted (05-0CT-2001) Psychiatry, Johns
Submitted (05-0CT-2001) R. Wolfe St., Baltimore,
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (human)
                                                                                                                                                                                                           YKSSTCYKRGGYYWGSKTCYSAGGKSRSMYYCMMRSSKSSSWSMSMARSSWCMGWGAGYR 17515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29056
GGGGCGCGTGGGGTCAGACCGCAAAGCGAAGGTGCGGGCCGGGGTGGGCCTCGCGGAGA
                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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/note="isolated from a patient with Huntington's
/noses-Like 2 (HDL2)"
complement(35581. 35746)
/rpt_type=tandem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /Product="junctophilin 3"
/product="junctophilin 3"
/product="junctophilin 3"
/product="junctophilin junctophilin junctoph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="synonym: JP3"
complement(<36507. .>36887)
/gene="JPH3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(<36507. .>36887)
/gene="JPH3"
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="junctophilin 3" complement(<36507. .36887)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="component of the junctional complex between membrane and endoplasmic reticulum"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="JPH3"
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224; Mismatches
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(JPH3) gene, partial cds.
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timore, MD 21287, USA
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REFERENCE
AUTHORS
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AP005772/c
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TITLE
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                              AL Submitted (25-SEP-2002) Takuji Sasaki, National Institute of Submitted (25-SEP-2002) Takuji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail:tsasaki@nlas.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7469)

NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* NOTE: This is a 'working draft' sequence.

* This sequence will be replaced

* the accession number will be preserved.

* the accession number will be preserved.

* Location/Qualifiers

1 179-630
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AP00577.2 GI:23491624
HTG; HTGS_PHASE2.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; En
Spermatophyta; Magnoliophyta; Liliopsida;
Ehrhartoideae; Oryzeae; Oryza.
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Oryza sativa (japonica cultivar-group) chi
OSJNBA0073a21, *** SEQUENCING IN PROGRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sasaki,T., Matsumoto,T. and Katayose,Y Oryza sativa nipponbare(GA3) genomic Diclone:OSJNBa0073A21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sasaki, T., Matsumoto, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Published Only in Database (2002)
2 (bases 1 to 172650)
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| TITLE Direct Submission Passearch Centre, JOURNAL Submission Sassoon Road, Pokfulam, Hong Kong FEATURES Location/Qualifiers  1.1279  /mol_type="genomic DNA" /db_xref="taxon:37727" /db_xref="taxon:37727" BASE COUNT 93 a 516 c 497 g 22 t 151 others ORIGIN  Query Match Best Local Similarity 45.3%; Pred. No. 0.046; Matches 231; Conservative 0; Mismatches 273; Indels 6; Gaps 2; | <b>3 2</b> | Db 91122 CGGGGCCCCNCCCGGGGCGGGGGGGGGGGGGGCCNNGCCGGCCGC 91080          | 448 GCCCGGCCGAGGCCGCCTCGAGGCCCGCGAGAGCCGGCTATAAAC 91182 CCCGGGGGCCGGCGGGGGGGGGGGGGGGGGGGGGCGGCG | Qy 388 CCGCAGCAGGAÁGTTGGCCAGGGCACGGCCGTGAGCGGAGCG | 334 AAGTCTCAAGCCCGGGCAAGGGAAAGGGGGCACGGGCTTCCCAAGGCCCGCCGGGCAAGGGAAAGGGGGCACGCCCCCGCGCGCCCCCGCGCGCCCCCC | Db         91422 GNNGGCGGGGCCCCGCGGGGGGGGGGGGGGGGGGGGG                                                        | QY 134 GGCCTGCCGTGCGCGAGGAAGCTCCTCACCAAAGCTCCCCTCACCAAAGCTCCCCTCACCAAAGCTCCCCTCACCAAAGCTCCCCTCACCAAAGCTCCCCCCCC | 94 GACGTTGCCACGGTCTGGGATCAGAGGCAGGGAGCCAGGGAGCCAGGAACTGCGCCCCCCCC | Matches 222; Conservative 0; Mismatches 295; Indels 6; Gaps 1;  Qy 34 CGTCCCTGGCGCCTCCACCTCCCCAGGCGCAGAAGGCGCCCAGAGGACCCCCAGTGCCC 93 |
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|                                                                                                                                                                                                                                                                                                                                                                                         |            | Search completed: September 20, 2003, 00:35:05 Job time: 2472.41 secs | <b>1</b> 55 80                                                                                  | 877 NCCCCNCGCGTGCGGCGCGCGGGCCCGCGCGCGCGCGCGCG     | 937<br>401                                                                                              | QY 281 GAGACAAAGGCCGGCCTGCCTCAGAGGGCCCCAGCGCCTGCCAAAAGGAAGTCCT 340 Db 997 CCGGCCCCCGGCCCCCCCCCCCGCGGGGGGGGGGG |                                                                                                                 |                                                                   | Qy 42 GCGCCTCCACCTCCCAGGCGCAGAAGGCGCCACAGAGGACCCCAGTGCCCGACGTTGC 101                                                                 |

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5 PCT-US91-06532-1
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             APPLICANT: rumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Enhang, Zemin
APPLICANT: Enhang, Zemin
ITILE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
ITITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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CURRENT PILING DATE: 1907-11-1-14
PRIOR APPLICATION NUMBER: 60/06787
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PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-12
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APPLICANT: Ashkenazi, Avi J.
APPLICANT: Botstein, David
APPLICANT: Botstein, David
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APPLICANT: Botstein, David
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Gerber, Hanspeter
APPLICANT: Geritsen, Mary E
APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Napier, Mary A.
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APPLICANT: Pan, James
APPLICANT: Stewart, Timothy
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Gerritsen, Mary E.
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Godowski, Paul J.
Grimaldi, J Christopher
Gurney, Austin L.
Kljavin, Tvar J.
Napler, Mary A.
Pan, James
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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GENERAL INFORMATION:
APPLICANT: Roizman, Bernard
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
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PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09
                                                                                                                                                                                                                                             TELEFAX: 312/984-9740
TELEFAX: 25-3856
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1335 base pairs
TYPE: NUCLEIC ACID
TYPE: NUCLEIC ACID
                                                                                                                           Matches
                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
ANAME: Gruber, Lewis S.
REGISTRATION NUMBER: 30,060
REFERENCE/DOCKET NUMBER: 2737
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/346-5750
TELEFAX: 312/984-9740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Rolzman, Bernaru
TITLE OF INVENTION: Recombinant Herpes St
TITLE OF INVENTION: Vaccines and Methods
TITLE OF RECURRICES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IPM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/06532
FILING DATE: 19910910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: Two Firs
CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 60603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Marshall, O'Toole, Gerstein, Murray ADDRESSEE: Bicknell
                                                                                                                                                                                                                        STRANDEDNESS: si
TOPOLOGY: linear
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                                                                                                                           al Similarity
169; Conserv
                                                                                  169 GCGAGGGAAGCTCCCTCACCNGAGGGAAGCTCCCCTCACCCGGCCCAGCCCTGCAGGGGG 228
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                                                           GEGCGAGAAGCCCACCCGCGGGGGGTCGCGGGGGTCGCGGGGGTCGCGGGGTCGCGG
                            GCGCGTGGGGTCAGACCGCAAAGCGAAGGTGCGGGCCGGGGTGGGCCTCGCGGAGACAAA 288
                                                                                                                                                                                                           TYPE:
Two First National Plaza
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                                                                                                                             Conservative
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                                                                                                                             Score 49.4; DB 5; Length 1
pred. No. 0.047;
0; Mismatches 182; Indels
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hes 0;
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                                                                                                                                                              Length 1335;
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US-09-103-840A-2
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GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: WHITE, Owen R.
APPLICANT: WENTER, John C.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DIA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM TITLE OF INVENTION: DIA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM TITLE OF INVENTION: UNBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION UNMBER: US/99/103,840A
CURRENT APPLICATION WIMBER: US/99/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOSTWARE: PATENTIN VET: 2.1
SEQ ID NO 2
SEQ ID NO 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 8.9%;
Best Local Similarity 46.7%;
Matches 231; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence OTHER INFORMATION: represent a, t, c or g
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                                                                                                                                                                                                  238 GTCAGACCGCAAAGCGAAGGTGCGGGCCGGGGTGGGCCTCGCGGAGACAAAGGCCCGGGCC
358 AGGGGGCACGGGCTTCCCAGGGCCCGCCGGCCGCAGCAGGAAGTTGGCCAGGGCA----
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                                                               TGCCTCTCTCAGAGGGCCCCAGCGCCTGCCAAGAGGAAGTCCTCGAGGCCCGGGCAGGGA 357
                                                                                                   GGCCGGCGGCAACGCCGGGACGCTCGCCACTGGTGATGGCGGGGGCCGGCGGGACCGGCGG
                                 CGCTAGTCGCAGCGGCGATTCGGCGGGGCAGGCGGAGCCGGCGACGCCGGCATGTT 841468
                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 48.8; DB 3;
Pred. No. 0.081;
0; Mismatches 253;
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Sequence 15, Application US/09128155

Patent NO. 6117654

GENERAL INFORMATION:
APPLICANT: PAN, Yang
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
FILE REFERENCE: 09404/052001
CURRENT APPLICATION UNMBER: US/09/128,155
CURRENT FILING DATE: 1998-08-03
EARLIER APPLICATION UNMBER: US 60/091,650
EARLIER FILING DATE: 1998-07-02
EARLIER FILING DATE: 1998-07-02
EARLIER APPLICATION UNMBER: US 60/054,646
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FEATSED FOR WINDOWS VERSION 3.0
LENGUETH: 152331
TYPE: DNA
ORGANISM: Homo Sapiens
                              RESULT 5
US-09-103-840A-1
Sequence 1, Application
Patent No. 6294328
GENERAL INFORMATION:
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NAME/KEY: misc_feature

LOCATION: (1)...(152331)

OTHER INFORMATION: n = A

US-09-128-155-16
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US-09-128-155-16/c
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                       CGGCGCTGGAGGÁGCGAGGACCGGGTATAAGAAGCCTCGTGGCCTTGCCCGGGCAGCCGC 520
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Pred. No. 0.079;
0; Mismatches 149; Indels 3;
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Sequence 14. Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
ITILE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                  RESULT 6
US-08-232-463-14/c
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; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA Mycobacterium tuberculosis
; OPHER INFORMATION: H37Rv
US-09-103-840A-1
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APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: FRASER, Claire M.
APPLICANT: PROBER CLAIRE M.
APPLICANT: PROBER CLAIRE M.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM TITLE OF INVENTION: TUBERCULOSIS
TITLE OF INVENTION: TUBERCULOSIS
TILLE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 198-06-24
NUMBER OF SEQ ID NOS: 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      470 AGGGGCGAGGACCGG 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      238 GTCAGACCGCAAAGCGAAGGTGCGGGCCGGGGGTGGGCCTCGCGGAGACAAAGGCCGGGCC 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTTCGGCTCCGGCGCCCCGCGCCCCCGCCGCCATTAGTAAAAGCGTCGGGGACAGCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGCCGGCGGGGCGGGGCCCCCGGGCTGATCGGCAACGGCGGCAACGGCGGCAACGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGGGGCACGGGCTTCCCAGGGCCCGCCGGCCGCAGCAGGAAGTTTGGCCAGGG-CACGGC 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGCCTCTCTCAGAGGGCCCCCAGCGCCTGCCAAGAGGAAGTCCTCGAGGCCCGGGCAGGGA 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGTGAGCGGAGCGGCAGGGCTTTC-----TCAGGAGCGGGGGGGGAGGCCGGCGCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGCCGGCGAACGCCGGGACACTCGCCACTGGTGATGGCGGGGCCGGGGGACCGGCGG 839230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAGGGACCAGGGAGCCAGGAACTGCGCCGCCCCCGCCCCTGCCCTGGCGCGAGGGAAGCT 180
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237 839170

60 838990

γQ Ъ QΥ В VΩ 밁 Qy 밁 δÃ В δÃ

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; CLONE: pTZgpt-F1s
US-08-232-463-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 433
PRIOR APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY,AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMM
REFERENCE/DOCKET NUMBER: 30472/114 IMM
TELECOMMUNICATION INFORMATION:
TELLEPHONE: (703)883-43109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGUTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
INMEDIATE SOURCE:
CLAURE: DTZGDT-F1s
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US-08-458-912-1/c
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Best Local S
Matches 13
                                                                                            Sequence 1, Application US/08458912
Patent NO. 5650310
GENERAL INFORMATION:
APPLICANT: Broer, Inge
APPLICANT: Hillemann, Doris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: VA
COUNTRY: USA
ZIP: 22313-0299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Watch 8.6%; Score 47.2; DB 1;
Local Similarity 4.4%; Pred. No. 0.14;
hes 13; Conservative 171; Mismatches 114;
                                    APPLICANT:
                                                                                                                                                                                                                                                                                                         1159
                                                                                                                                                                                                                                                                                                                                                                    1099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 223 AGGGGGGGGGGGGGGGAGAGCGAAAGCGAAGGTGCGGGCCGGGGTGGGCCTCGCGGA 282
                                                                                                                                                                                                                                                                                                                                                                                                  283 GACAAAGGCCGGGCCTGCCTCTCTCAGAGGGCCCCAGCGCCTGCCAAGAGGAAGTCCTCG 342
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USA
NT: Donn, Gunter
NT: Mullner, Hubert
NT: Bartsch, Klaus
F INVENTION: DEACETYL
                                                                                                                                                                                                                                                                                                                                       GGCCAGGGCACGGCCGTGAGCGGAGCGGGCAGGGCTTTCTCAGGAGCGCGGGGCGAGGCCG 462
                                                                                                                                                                                                                                                                       GCGCTGGAGGGCGAGGACCGGGTATAAGAAGCCTCGTGGCCTTGCCCGGGCAGCCGC 520
                                                                                                                                                                                                                                                                                                         RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRATCGCAAGCTCCCTCGACCTGCAGC 1042
                                                                               Hillemann, Dor
Puhler, Alfred
                                                                  Wohlleben, Wolfgang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US/08/232,463
       Klaus
DEACETYLASE GENES FOR THE PRODUCTION
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TOPOLOGY: US-08-458-912-1
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REGISTRATION NUMBER: 28,029
REFERENCE/DOCKET NUMBER: 5144.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 932 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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RESULT 8
US-08-461-179-1/c
US-08-461-179-1/c
; Sequence 1, Application US/08461179
; Patent No. 5668297
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 1036

COMPUTER READABLE FORM:

COMPUTER READABLE FLOPPY disk

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC COMPATIBLE

COMPUTER: IBM PC COMPATIBLE

COPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1

SOFTWARE: PatentIn Release #1.0, Version #1

CURRENT APPLICATION DATA:

APPLICATION UNUMBER: US/08/458,912

FILING DATE: 02-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION UMBER: US 07/926,498

APPLICATION NUMBER: US 07/926,498

ETLING DATE: 07-AUG-1992

ATTORNEY/AGENT INFORMATION:

NAME: Lawrence, William F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: PHO
TITLE OF INVENTION: PHO
TITLE OF INVENTION: PRO
TITLE OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 550 CITY: New York STATE: New York STATE: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Curtis, Morris & Safford ADDRESSEE: c/o William F. Lawrence
                                                                                                                                                                                                                                                                                                                                                                                                                                                   744 TOGTOGTACAGGACTTCCTCGGAACCGACCTGGATGAGCAGGGGGGGCAGACCGGTCAGA 685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 624
                                                                                                                                                                                                                                                                                                                                                                                    684 TCGCCGTGGGCGGGCGAGGCCAGGGGGTTCCTGGGATCGGTGCCGGCCAGGTAGCGCCCC
                                                                                                                                                                                                                                                                                                                                                                                                        424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      164;
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                                                                                                                    444
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Similarity 48.5%;
64; Conservative (
                                                                                                                                                                                                                                                                                                                  GCCATGCGGAGCAGGTCCTCGGTGTCCAGGAGGATCTCGCGCTCCTTGCGGGTGACGTGC
                                                                                                                                                                                                                                                                                                                                                TCTCAGAGGGCCCCAGCGCCTGCCAAGAGGAAGTCCTCGAGGCCCGGGCAGGGAAGGGG
                                                                                                                                                                                                                                                   TCACCGGCGAAGGTGATCCGCCCGGCGGCAGGCCCCG
                                                                                                                                                CGAGGACCGGGTATAAGAAGCCTCGTGGCCTTGCCCGG 512
                                                                                                                                                                                                                   GGAG-------CGGGCAGGGCTTTCTCAGGAGCGCGGGCGAGGCCGGCGCTGGAGGGG 474
                                                                                                                                                                                  single المحدد
linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              514410-2882
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pred. No. 0.17;
0; Mismatches 165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #1.25
                                                                                                                        407
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APPLICANT:

Broer, Inc

Doris

NUMBER OF SEQUENCES: 1

COUNTRY: Ut ZIP: 10036

Дb

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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC| compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIN Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/461,179

FILING DATE: 07-AUG-1992

PRIOR APPLICATION NUMBER: US 07/926,498

FILING DATE: 07-AUG-1992

APPLICATION NUMBER: US 07/926,498

FILING DATE: 07-AUG-1992

APPLICATION NUMBER: US 07/926,498

FILING DATE: 07-AUG-1992

APPLICATION NUMBER: US 07/926,498

FILING DATE: 07-AUG-1992

APPLICATION NUMBER: 138,029

REFERENCE/DOCKET NUMBER: 514410-2882

TELEPHONE: (212) 840-0712

TELEPHONE: (212) 840-0712

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS: LEMTH: 932 DASE PAIRS

TYPE: nucleic acid

STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Wohlleben, Wolfgang
APPLICANT: Donn, Gunter
APPLICANT: Mullner, Hubert
APPLICANT: Bartsch, Klaus
TITLE OF INVENTION: DEACETYLASE GENES FOR THE PRODUCTION OF
TITLE OF INVENTION: PHOSPHINOTHRICIL OR
TITLE OF INVENTION: PHOSPHINOTHRICYL-ALANYL-ALANINE,
TITLE OF INVENTION: PROCESSES FOR THEIR ISOLATION, AND THEIR USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Curtis, Morris & Safford
ADDRESSEE: c/o William F. Lawrence
STREET: 530 Fifth Avenue
CITY: New York
STATE: New York
                           475 CGAGGACCGGGTATAAGAAGCCTCGTGGCCTTGCCCGG 512
                                                                                                                                                                                                                                                                                                                   GAGGCGCCCTCGCAGGCCAGGTCGGCCCAGGGCGAGATGCACACCGCGGCGGCGGCAGC
                                                                                                                                                                                    CACGGGCTTCCCAGGGCCCGCCGCCGCCAGCAGCAGGTTGGCCAGGGCAGGCCAGGCCGTGAGC
                                                                                                    GCCATGCGGAGCAGGTCCTCGGTGTCCAGGAGGATCTCGCGCTCCTTGCGGGTGACCTGC 565
                                                                                                                                                                                                                                                  TCTCAGAGGGCCCCAGCGCCAGGCAAGAGGAAGTCCTCGAGGCCCGGGCAGGGAAGGGGG
                                                                                                                                                                                                                                                                                               TCCCCGTGGGCGAGGCCAGGGGGTTCCTGGGATCGGTGCCGGCCAGGTAGCGCCCC
                                                                                                                                                                                                                                                                                                                                                                  United States of America
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 46.6; DB 1; Length 932; 
Pred. No. 0.17;
0; Mismatches 165; Indels 9;
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MEDIUM TYPE: Floppy disk
COMPUTER IBM CC COMPATIBLE
COMPUTER: IBM CC COMPATIBLE
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Vers
APPLICATION DATA:
APPLICATION UNMBER: US/08/459,254
FILING DATE: 02-7UN-1995
PRIOR APPLICATION NUMBER: US 07/926,498
FILING DATE: 07-AUG-1992
APPLICATION NUMBER: US 07/926,498
FILING DATE: 07-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: LAWFENCE, William F.
REFERENCE/DOCKET NUMBER: 51,410-288;
TELEPHONE: (212) 840-333
TELEPHONE: (212) 840-333
TELEPHONE: (212) 840-7712
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 932 base pairs
TYPE: Nucleic acid
CTT DANNEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                US-08-459-254-1
                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 48.5
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US-08-459-254-1/c
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; Patent No. 576;
; GENERAL INFORM
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: MAILNET, HUBERT
APPLICANT: BARTSCH, KLAUS
TITLE OF INVENTION: DEACETYLASE GENES FOR THE PRODUCTION
TITLE OF INVENTION: PHOSPHINOTHRICIN OR
TITLE OF INVENTION: PHOSPHINOTHRICYL-ALANINE,
TITLE OF INVENTION: PROCESSES FOR THEIR ISOLATION, AND TH
UNMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 530 Fi
CITY: New York
STATE: New Yor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Curtis, Morris & Safford ADDRESSEE: C/O William F. Lawrence STREET: 530 Fifth Avenue
364 CACGGGCTTCCCAGGGCCCGCCGGCCGCAGCAGGAGTTGGCCAGGGCACGCCGTTGAGC
                                                     624 GCCATGCGGAGCAGGTCCTCGGTGTCCAGGAGGATCTCGCGCTCCTTGCGGGTGACGTGC
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CANT: Broer, Inge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1, Application US/08459254
o. 5767370
                                                                                 TCTCAGAGGGCCCCAGCGCCAGAGAGGGAAGTCCTCGAGGCCCGGGCAGGGAAGGGGG
                                                                                                                          TCCCCGTGGGCGGGCCAGGCCAGGGGTTCCTGGGATCGGTGCCGGCCAGGTAGCCCCCC
                                                                                                                                                  New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       United States of America
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Puhler, Alfred
Wohlleben, Wolfgang
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                                                                                                                                                                                                                                                                            8.5%; Score 46.6; DB 1;
48.5%; Pred. No. 0.17;
ative 0; Mismatches 165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gunter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                              Length
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                                                                                                                              625
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Qγ Dδ Qy

504 424 564 364 624 304 684

DЬ δÃ Ър δÃ Ъ δÃ

US-08-461-179-1

Query Match Best Local Similarity Matches 164; Conserv

Conservative

Вр VΩ

Qy

RESULT 10 US-08-459-255-1/c

Sequence 1, Application US/08459255 Patent No. 5767371 GENERAL INFORMATION:

| NNORMATION: Inge NN: Hillsman Altred NN: Hillsman Altred NN: Dillsman Nordian NN: Hillsman Altred NN: Dillsman Nordian NN: Dillsman Nordian NN: Dillsman Nordian NN: Dillsman Nordian NN: Dillsman Nordian NN: DexCETVLANE GENES FOR THE PRODUCTION OF NUMBRION: PHOSPHINOPHRICIL NORDIAN PROVENTION: PHOSPHINOPHRICIN NAND THEIR USE OF INVENTION: PHOSPHINOPHRICIN NAND THEIR USE OF INVENTION: PHOSPHINOPHRICIA OF SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCES: 1 OP SEQUENCE | ULT 10 09 08-459-255-1/c 09 08-459-255-1/c 09 08-459-255-1/c 09 08-459-255-1/c 09 08-459-255-1/c 09 09 08-459-255-1/c 09 09 09 09 09 09 09 09 09 09 09 09 09 | 564 GAGGCGCCTCGCAGGCCAGGTCGGCCCAGGGCGAGATGCACACCGCGGCCGGC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | Sep 22 15:31:38 2003 |
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COMPUTER READABLE FORM:

MEDIUM TYPE: Flöppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/814,095
FILING DATE:
CLASSIFICATION: |800
ATTORNEY/AGENT INFORMATION:
NAME: MONTGOMER: 38,972
REFERENCE/DOCKET NUMBER: 2391.00066
TELECOMMUNICATION INFORMATION:
TELEPHONE: (248) 539-5055
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 35060 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPPLOGY: linear |
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Cosmid including ACHE DESCRIPTION: promotor, ACHE gene and ARS gene"
HYPOTHETICAL: NO
ORIGINAL SOURCE:
OPERATION SOURCE: Nome and ARS gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 12
US-08-814-095-7
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Patent No. 6025183
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Zakut, Haim
APPLICANT: Shani, Moshe
TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR
TITLE OF INVENTION: ANTI-CHOLINESTERASE SUBSTNACES
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                          ORGANISM: Homo sapiens POSITION IN GENOME:
                                                                                                                                                         CHROMOSOME/SEGMENT:
FEATURE:
                                                NAME/REY: promoter LOCATION: 4089.22464
OTHER INFORMATION: //function= "ACHE Promotor"
OTHER INFORMATION: //standard_name= "ACHE Promotor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: KOHN & ASSOCIATES
STREET: 30500 No. 6025183thwestern Highway, Suite
CITY: Farmington Hills
STATE: Michigan
        NAME/KEY: exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      155
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IOANTION: 24090...25177

LOCATION: 24090...25177

IDENTIFICATION METHOD: experimental

OTHER INFORMATION: /function= "(translation start:
OTHER INFORMATION: /24110)"

OTHER INFORMATION: /evidence= EXPERIMENTAL
OTHER INFORMATION: /gene= "ACHE"

OTHER INFORMATION: /number= 2

FEATURE: exon
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LOCATION: 25524...26009
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OTHER INFORMATION: /gene= "ACHE"
OTHER INFORMATION: /gene= "ACHE"
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RAME/KEY: exon

LOCATION: complement (34528..34895)

OTHER INFORMATION: /function= "arrenit

OTHER INFORMATION: gene= "AR"

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NAME/KEY: exon

LOCATION: complement (34092..34358)

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FEATURE:

NAME/KEY: exon

LOCATION: complement (33779..33963)

OTHER INFORMATION: /gene= "AR"

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LOCATION: 27255..28007
LDENTIFICATION EMTHOD: experimental
OTHER INFORMATION: /evidence= EXPERIMENTAL
OTHER INFORMATION: /gene= "ACHE"
OTHER INFORMATION: /number== 5
FEATURE:
NAME/KEY: terminator
NAME/KEY: 72965 27387
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LOCATION: 28008..28129
LDENTIFICATION METHOD: experimental
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FEATURE:
                                                                            LOCATION: complement (33493..3591)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
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LOCATION:
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OTHER INFORMATION: /number= 1
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LOCATION: 27005..27274
                                                      NAME/KEY: exon
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28129..28131
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/number=

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NAME/KEY: exon
LOCATION: complement (29664..29856)
OTHER INFORMATION: /gene= "ARS"
OTHER INFORMATION: /number= 16
US-08-814-095-7
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Best Local Similarity 46.8%;
Matches 176; Conservative
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EATURE:
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LOCATION: complement (30816..31011)
OTHER INFORMATION: /gene="AR"
OTHER INFORMATION: /number= 12
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HER INFORMATION: /gene- "AR"
HER INFORMATION: /number= 7
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                                   271 GGGCCTCGCGGGGAGACAAAGGCCGGGCCTGCCTCTCTCAGAGGGGCCCCAGCGCCTGCCAAG 330
                                                                                                          GCCCAGCCCTGCAGGGGGGCGCGTGGGGTCAGACCGCAAAGCGAAGGTGCGGGCCGGGGT 270
                                                                         GCTGCCAATAAACTGTTACAGCCACGGGAGTGTGCGCGACTAGGGAGCCCAGGGGTAGAGG
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                                                                                                                                                                                                                              Score 45.8; DB 3;
Pred. No. 0.28;
0; Mismatches 198;
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                                                                                                                                                                                                                                                                        Length 35060;
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210

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US-08-483-533-4
                                                                                                     TYPE: nucleic STRANDEDNESS: TOPOLOGY: lin MOLECULE TYPE: US-08-483-533-4
                                                                                                                                    TELLER: 314,
TELERS: 25-3856
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SEQUENCE CHARACTERISTICS: 25-3856
SEQUENCE CHARACTERISTICS: 25-3856
SEQUENCE CHARACTERISTICS: 25-3856
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
              QΥ
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                                              Query Match
Best Local S
Matches 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                          ATTORNEY AGENT INFORMATION:
NAME: Zeller, James P.
REGISTRATION NUMBER: 28,491
REFERENCE/DOCKET NUMBER: 2809
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21F: bubou CAPERINE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Roizman, Bernard
APPLICANT: Chou, Joany
TITLE OF INVENTION: Method fo
TITLE OF INVENTION: Diseases
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/419,853
FILING DATE: 11-APR-95
PRIOR APPLICATION NUMBER: 07/861,233
FILING DATE: 31-MAR-92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Rel
                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US, FILING DATE: 07-MAR-95 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 6300 :
CITY: Chicago
STATE: Illino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28445 AGGCGAGCTCCGAGGCGGGCGCAAGGCAAAGGCCAACCCCTAGCCCTGCCCTGCCGGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: United States of America ZIP: 60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28625 CTCGGTCGGTGCCGGT 28640
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                                       8.2%; al Similarity 46.2%; 183; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , Application US/08483533 6172047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CGCGGGCGAGGCCCTGGAGGGGCGAGGACCGGGTATAAGAAGCCTCGTGGCCTTGC 508
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TGAGGCCTGATCGTGGCGCCTCCACCTCCCCAGGCGCAGAAGGCGCCCACGAGAG
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                                                                                                                  linear
E: DNA (genomic)
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                                                Score 45:4; DB 3;
Pred. No. 0.3;
0; Mismatches 212;
                                                                                                                                                                                                                                                                                            28097/32742
                                                                                  Length 595;
                                                       Indels
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                                                         Gaps
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RESULT 14
US-09-283-471A-4
                                                                                                                                COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIAL Release #1.0, Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/99/283,471A
FILING DATE: 04-APR-1999
CLASSIFICATION: 514
APPLICATION UMBER: 07/861,233
FRIOR APPLICATION DATA:
APPLICATION UMBER: 08/419,853
FILING DATE: 31-ARR-1992
PRIOR APPLICATION UMBER: 08/419,853
FILING DATE: 11-APR-1995
APPLICATION NUMBER: 08/483,533
FILING DATE: 07-UN-1995
APPLICATION NUMBER: 28/491
APPLICATION NUMBER: 28/491
APPLICATION NUMBER: 28/491
REGISTRATION NUMBER: 28/491
REGISTRATION NUMBER: 27373/32742A
TELEPONE: 312/474-6300
TELEPAX: 312/474-0448
TELEPAX: 312/474-0448
                                                                              TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4, Application US/09283471A Patent No. 6340673 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Roizman, Bernard
APPLICANT: Chou, Joany
TITLE OF INVENTION: Method For Treating Tumorigenic Diseases
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illnois
Third States of America
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatt)
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SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                           28,491
RER: 27373/32742A
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Patent No. 6172047
GENERAL INFORMATION:
APPLICANT: Roizman, B
APPLICANT: Chou, Joan
TITLE OF INVENTION: M
TITLE OF INVENTION: D
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 15
US-08-483-533-36
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; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-283-471A-4
                              COUNTRY: United States of America
ZIP: 60605-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vei
COMPUTER: US/OB/483,533
FILING DATE: 07-MAR-95
FILING DATE: 07-MAR-95
PRICATION UMBER: 08/419,853
FILING DATE: 11-APR-95
PRIOR APPLICATION DATA:
APPLICATION UMBER: 07/61,233
FILING DATE: 11-ARR-95
PRIOR APPLICATION LOWBER: 07/861,233
FILING DATE: 11-ARR-95
PRIOR APPLICATION LOWBER: 07/861,233
FILING DATE: 31-MAR-95
PRIOR APPLICATION LOWBER: 07/861,233
FILING DATE: JI-MAR-95
PRIOR APPLICATION LOWBER: 07/861,233
PRIOR APPLICATION LOWBER: 07/861,233
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STREED:
CLIY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
ZIP: FORM:
PRADDABLE FORM:
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Best Local S
              NAME: Zeller, James REGISTRATION NUMBER:
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ADDRESSEE: Marshall, O'Toole,
STREET: 6300 Sears Tower, 233
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183; Conservative
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James P. 28,491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Joany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Method for Treating Tumorigenic Diseases
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Pred. No. 0.3;
0; Mismatches 212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gerstein, Murray &
South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 595;
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REFERENCE/DOCKET NUMBER: 28097/32742

TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 1327 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-483-533-36
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Search completed: September 20, 2003, 01:41:14 Job time: 89.9316 secs
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                                                                                                                                                                                                                                                                                                                                                                                                              203 CTCACCCGGCCCAGCCCTGCAGGGGGGGGGGGGGTCAGACCGCAAAGCGAAGGTGCGG 262
671 ACCCCCGCGAACCCCCGCGACCCCCGCGCGGGGGGGGGTGCGCTTCTCGCCCCACGTCCGGGTGCGC 730
                                                                                                                                                                                                                                                                                            791
                                                                                                                                                                            TGCCTGGGGCCCGAGGCCCGTGCCCGGGCCCTGGCC 886
                                                                                        CGCCGGCCGCAGCAGGAAGTTGGCCAGGGCACGGCC 417
                                                                                                                   CGGGCCGACCGGGCTCGGTTCCGGCGCCGGGTGGCGGAGGCGGTCATCGGGCCG 850
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Title:
Perfect score:
Sequence:

US-10-081-817A-19 551 1 cggccggggaggcgg

cggccgggaggcggccggg.....

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Scoring table:

IDENTITY\_NUC Gapop 10.0 ,

Gapext 1.0

Minimum DB seq Maximum DB seq

length: 0 length: 2000000000

of

hits satisfying

chosen parameters:

2552756 seqs, 1349719017 residues

Post-processing: Minimum Match Maximum Match

Listing first 45 summaries

100%

Database

Result No.

Score

Query Match

Length

DB

Ħ

Description

SUMMARIES

8765442

298.4 120 117 92 92 78 78 78

1794 562 190 543 543 519 569 570

24 19 19 21 21 19 24 24

ABT06542 AAV54620 AAV54616 AAZ98173 AAZ29723 AAX29723 AAV54621 ABK40267 AAZ65103

OM nucleic - nucleic search, using sw

Copyright

GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd

September 19,

2003,

23:14:28 ; model

on:

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                    N_Geneseq_19Jun03:*

1: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*

2: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*

3: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*

4: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*

5: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:*

5: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*

6: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*

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12: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*

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25: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001.BAT:*

26: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001.DAT:*

27: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001.DAT:*

28: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001.DAT:*

29: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001.DAT:*
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Membrane-bound pro
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ID ABT0
AC ABT0
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KW retL
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                                                                                                                                                                                                                                                                                                         gene;
                                                                                                                                                                                                                                                                                                                        Human; methylated gene; methylation; breast cancer; marker; WT-1; cell proliferative disorder; TWIST; HOXA5; NES-1; RARbeta; cyclin D2; retinoic acid receptor beta; oestrogen receptor; Wilms' tumour; 14.3.3 sigma; HIN-1; RASSFIA; tumour suppressor gene; hypermethylation;
                                                                                                                                                                                                                                                                                                                                                                                                                       Human HIN-1 coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABT06542;
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                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                             (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
                                                                                                                                                        28-JAN-2002; 2002WO-US02455
      WPI; 2002-599803/64
                                                                                                                   26-JAN-2001; 2001US-0771357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49
                                                                                                                                                                                                                                                                                                           promoter;
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10.6 43058

10.6 14958

10.5 114955

10.1 629

10.1 3743

9.1 17213

9.1 33537

9.0 11237

8.9 12561

8.9 22561

8.9 31985

8.8 31985

8.8 4411529

8.7 154746

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ABX17173

ABX17173

ABX153491

ABF1080

AAX53491

ABH164982

ABH165219

ABH165219

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ABM613151

ABM613171

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AAX09974
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                                                  Sacchi N,
                                                     Davidson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human PRO1245 (UNQ Novel human secreted/tra Human secreted/tra Human secreted/tra Human secreted/tra Human secreted/tra Human secreted/tra Human PRO polynucl Human PRO polynucl Human PRO polynucl LU105 specific pol Human breast cance Human breast cance thuman adenosine Al Gene #3953 used to Lung cancer relate Human adenosine Al Gene #3953 used to Lung cancer relate Human adenosine Al Oligonucleotide fo Oligonucleotide fo Oligonucleotide fo Oligonucleotide fo Human mast cell re HSV-2 strain SB5 C Human secreted pro HSV-1 (F) ICP34.5 Human Colon cancer Rabbit low density Mycobacterium tube HSV-2 immediate ea Human herpesvirus Human herpesvirus Human herpesvirus Human herpesvirus Human low density Novel protein kina Human low density Human Indoord genomi
                                                         ž
                                                         Fackler MJ;
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RESULT 2
AAV54
AC AAV5
XX
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C 25-M
DT 30-C
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DE LU10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local :
Key
                                                                                                                 LU105; lung disease marker; blood; plasma; serum; ss.
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                                                             Homo sapiens.
                                                                                                                                                                                                          LU105 specific consensus polynucleotide sequence
                                                                                                                                                                                                                                                                        25-MAR-2003
30-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                              AAV54620 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1794 BP; 240 A; 646 C; 522 G; 318 T; 68 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tch | 54.2%; Score 298.4; al Similarity | 92.6%; Pred. No. 2.6 302; Conservative 0; Mismatches
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   Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                              562
                                                                                                                                                      immunoassay;
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RESULT 3
AAV54616
ID AAV5
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AC AAV5

AAV54616 standard; cDNA; 190

AAV54616;

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Вb
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                                                                                                                                                         В
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                                                                                                                                                                                                                                                                                                                   Sequences shown in AAV54616 to AAV54621 represent LUIO5 specific
CC polynucleotide sequences. These are used in the method of the invention
CC for detecting target LUIO5 nucleic acid. The method comprises treating a
CC sample with at least one LUIO5 specific nucleic acid, or its complement
CC which is at least 50 percent identical with the LUIO5 specific nucleic
CC acid sequences (AAV54616 to AAV54621). LUIO5 is a lung disease marker.
CC cells transformed with a recombinant expression system that contains
CC LUIO5 specific nucleic acid fragments, are used to express recombinant
CC LUIO5 specific nucleic acid fragments, are used to express recombinant
CC used to detect the LUIO5 antigen, and correspondingly this antigen is
CC used to detect specific antibodies, in usual immunoassays. The LUIO5
CC polypeptides and nucleic acid sequences are used for diagnosis, staging,
CC used to detect specific antibodies, in usual immunoassays. The LUIO5
CC polypeptides and nucleic acid sequences are used for diagnosis, staging,
CC used to detect typecific antibodies, in usual immunoassays. The LUIO5
CC polypeptides and nucleic acid sequences are used for diagnosis, staging,
CC used to detect typecific antibodies, in usual immunoassays. The LUIO5
CC polypeptides are also used to screen for specific binding agents, useful
CC therapeutically. LUIO5 is a marker for lung disease (present at high
CC concentration, in altered form or in an unusual body compartment). LUIO5
CC can be detected in blood, plasma or serum in an inexpensive, non-invasive
                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid for the lung disease marker LU105 - polypeptides, antibodies and genes, used for diagnosis, prevention, treatment of lung disease, specifically cancer
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P-PSDB; AAW75868.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDS
                                                                                                                                                                                                                                                                                                                   Sequence 562 BP; 82 A; 200 C; 192 G; 86 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-AUG-1998
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                                                                                                                                                       551 C 551
                                                                                                                   491
                                                                            61
                                                                                                                                                                                                                                        120;
                                                                                                                                                                                                                                      21.8%; Score 120; DB 19; Length 562; Similarity 99.2%; Pred. No. 1.1e-14; 20; Conservative 0; Mismatches 1; Indels
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ი -
                                                                                                 GAAGCCTCGTGGCCTTGCCCGGGCAGCCGCAGGTTCCCCGGCGCCCCGAGCCCCCGCGC
                                                                            GAAGCCTCGTGGCCTTGCCCGGGCAGCCGCAGGTTCCCCGCGCGCCCCGAGCCCCCGCGC
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/*tag= a

/transl_except= (pos:176..178, aa:Val)

/product= "LUI05 polypeptide"
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Robertsrapp L;
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CC golynucleotide sequences. These are used in the method comprises treating a general surject LUIO5 nucleic acid. The method comprises treating a CC for detecting target LUIO5 nucleic acid. The method comprises treating a CC sample with at least one LUIO5 specific nucleic acid, or its complement acid sequences (AAV54616 to AAV54621). LUIO5 is a lung disease marker. CC cells transformed with a recombinant expression system that contains CC LUIO5 specific nucleic acid fragments, are used to express recombinant CC LUIO5 specific nucleic acid fragments, are used to express recombinant CC LUIO5 polypeptides which are used to raise antibodies. The antibodies are CC used to detect the LUIO5 antigen, and correspondingly this antigen is CC used to detect specific antibodies, in usual immunoassays. The LUIO5 CC used to detect specific antibodies, in usual immunoassays. Staging, polypeptides and nucleic acid sequences are used for diagnosis, staging, CC polypeptides are also used to screen for specific binding agents, useful concentration, in altered form or in an unusual body compartment). LUIO5 CC can be detected in blood, plasma or serum in an inexpensive, non-invasive cc test.
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30-OCT-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid for the lung disease marker LU105 - polypeptides, antibodies and genes, used for diagnosis, prevention, treatment of lung disease, specifically cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ABBO ) ABBOTT LAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 11; Fig 1; 123pp; English
                                                                                                                                                                                                        Sequence 190
                                                                                                                                                                                                                                (Updated on 25-MAR-2003 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                specific polynucleotide sequence from clone 3353867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lung disease marker; immunoassay; lung disease; cancer;
plasma; serum; ss.
                                                                                                al Similarity
117; Conserv
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                       551 C 551
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(first entry)
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                                                                                                                                                       Conservative
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ges SC,
upe SD;
                                                                                                                                                                                                         A; 69 C; 67 G;
                                                                                                                                                                    21.2%;
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Klass MR, Kratochvil JD, Rob
                                                                                                                                                                                                                                     correct PI field.)
                                                                                                                                                         0;
                                                                                                                                                                     Score 117; DB 19;
Pred. No. 4.3e-14;
                                                                                                                                                           Mismatches
                                                                                                                                                                                                              32 T; 4 other;
                                                                                                                                                            4;
                                                                                                                                                                                   Length 190;
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                                                                                                                                                              0;
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                AX AAZ98109 to AAZ98242 encode AAY87224 to AAY87357 which represent the cc human signal peptide-containing proteins HSPP-1 to HSPP-134. HSPPs have anticancer, anti-inflammatory, antimicrobial, noctropic, hepatotropic, anticancer, anti-inflammatory, antimicrobial, noctropic, hepatotropic, according to the decreased decreased and antiasthmatic activities, and can cell seed in gene therapy. HSPPs can be used to treat or prevent disorders associated with increased cell HSPP are used to treat or prevent disorders associated with increased cell HSPP are used to treat or prevent disorders associated with increased cell HSPP are used to treat or prevent disorders. (c. (including cancer), inflammation, cardiovascular, neurological, cell-trhosis, psoriasis, acquired immune deficiency syndrome, anaemia, cell-trhosis, congestive or cell-trhosis, psoriasis, acquired immune deficiency syndrome, anaemia, cell-trhosis, congestive or cell-trhosis, psoriasis, acquired immune deficiency syndrome, anaemia, cell-trhosis, congestive or cell-trhosis, schizophrenia, ovulatory defects, muscular dystrophy). HSPP for nucleic acids can be used for the recombinant production of HSPP, for cell-tel-cell-tracetion and amplification assays (for cell-tel-cell-tracetion and amplification are also used to cell-tracetion and amplification are also used to cell-tracetion and amplification are also used to cell-trace
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31-JUL-1998;
01-OCT-1998;
11-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New human signal peptide-containing proteins useful in treatment, prevention and diagnosis of e.g. cancer, inflammation and cardiovascular disease -
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DB; AAY87288.
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98US-0094983.
98US-0102686.
98US-0112129.
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Yue
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R, Hillman
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RRESULT 5
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Matches 92
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Best Local
                                                                                                                                                                                                                                                         The present sequence is a lung specific gene (LSG) Lng107 from human clone ID 586271. The LSG has high level of tissue specificity for lungs and is overexpressed in cancerous tissues. The sequence serves as a diagnostic marker for detecting, monitoring, staging and prognosticating lung cancer. The diagnosts involves comparing levels of LSG in samples obtained from patient and normal control.
                                                                                                                                                                                                                                                                                                                                                                                                     Claim 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                     A new method for diagnosing, monitoring and staging lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-116320/10.
P-PSDB; AAY44458.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yang F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lung Specific Gene;
prognosticate; lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAZ29723 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 543 BP;
                                                                                                                                                                                                                       Sequence 543 BP; 89 A; 194 C; 178 G; 82 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-мат-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human lung specific
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (DIAD-)
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                         520
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
                                                                                                                                              l Similarity
92; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 μ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DIADEXUS LLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Macina RA,
  CAGGTTCCCCGCGCGCCCCGAGCCCCCGCGCCC
                                                                                  CCGGCGCTGGAGGGCCGAGGACCGGGTATAAGAAGCCTCGTGGCCCTTGCCCGGGCAGCCG
                                                                                                                                                                                                                                                                                                                                                                                                 Page 36; 40pp; English.
                                                                CCGGCGCTGGAGGGCGAGGACCGGGTATAAGAAGCCTCGTGGCCTTGCCCGGGCAGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAGGTTCCCCGCGCGCGCCCGAGCCCCCGCGCC
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                                                                                                                                           Conservative
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/product=
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93..407
/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16.7%; 50
100.0%; Pr
                                                                                                                                  16.7%; 50
100.0%; Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LSG; Lng107; human; cancer; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene Lng107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; 194 C; 178 G; 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "LSG Lng107 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 92; DB 21;
Pred. No. 2.9e-09;
                                                                                                                                                           Score 92;
Pred. No.
                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                           DB 21;
0. 2.9e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         diagnostic marker;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T; 0 other;
                      551
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                                                                                                                                           0,;
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                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          cancer
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                                                         밁
                                                                                                                                Sequences shown in AAV54616 to AAV54621 represent LU105 specific
CD polynucleotide sequences. These are used in the method of the invention
CD for detecting target LU105 nucleic acid. The method comprises treating a
CD sample with at least one LU105 specific nucleic acid, or its complement
CD which is at least 50 percent identical with the LU105 specific nucleic
CD cold sequences (AAV54616 to AAV54621) LU105 is a lung disease marker.
CD cells transformed with a recombinant expression system that contains
CD cold specific nucleic acid fragments, are used to express recombinant
CD cold specific nucleic acid fragments, are used to express recombinant
CD cold specific nucleic acid fragments, are used to express recombinant
CD used to detect the LU105 antigen, and correspondingly this antigen is
CD used to detect specific antibodies, in usual immunoassays. The LU105
CD polypeptides and nucleic acid sequences are used for diagnosis, staging,
CD monitoring, prognosis, prevention, treatment and determination of
CD susceptibility to, lung disease, specifically cancer. The LU105
CD polypeptides are also used to screen for specific binding agents, useful
CD concentration, in altered form or in an unusual body compartment). LU105
CD concentration, in altered form or serum in an inexpensive, non-invasive
CD can be detected in blood, plasma or serum in an inexpensive, non-invasive
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid for the lung disease marker LU105 - polypeptides, antibodies and genes, used for diagnosis, prevention, treatment of lung disease, specifically cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Billing-medel PA, Co
Granados EN, Hodges
Russell JC, Stroupe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 11; Fig 1; 123pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LU105; lung disease marker; blood; plasma; serum; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAV54621;
                                                           Sequence
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30-OCT-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1998-437479/37.
DB; AAW75868.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 CAGGTTCCCCGCGCGCGCCCCGAGCCCCCGCGCC 92
                                                                                                  on 25-MAR-2003 to correct PI field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (updated)
(first entry)
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jes SC,
ipe SD;
                                                           A; 190 C; 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      M, Colpitts TL, Friedman Klass MR, Kratochvil JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA clone 1327836IH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immunoassay; lung disease; cancer;
  Score 78;
Pred. No.
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                                                           G; 81
    DB 19;
1.5e-06;
                                                           T; 0 other;
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                      Length 519;
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Robertsrapp L;
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Matches

78;

Conservative

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474

밁 VΩ В δõ

534 61

GCCCGAGCCCCGCGCC 78
GCCCCGAGCCCCCGCGCC 78

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15-JUL-2002 ABK40267;

(first entry)

cDNA encoding human PRO1245

ABK40267 standard; cDNA; 569

ВP

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Human; PRO; benign tumour; malignant tumour; lymphoid malignancy; leukaemia; neuronal disorder; stromal disorder; blastocoelic disoinflammatory disorder; immune disorder; angiogenic disorder; gene therapy; cytostatic; neuroprotective; gene; ss.
The present invention relates to the isolation of novel human PRO polypeptides and the polynucleotide sequences encoding them. The PRO polypeptides, agonists, antagonists or anti-PRO antibodies are useful for treating benign or malignant tumours (e.g. renal, kidney, bladder, breast, etc), leukaemias and lymphoid malignancies, other disorders such as neuronal, glial, astrocytal, hypothalamic, glandular,
                                                                                                                   Thirty five nucleic acids encoding PRO polypeptides, useful for treating benign or malignant tumours, leukaemias and lymphoid malignancies, inflammatory, angiogenic and immunologic disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCGAGGACCGGGTATAAGAAGCCTCGTGGCCTTGCCCGGGCAGCCGCAGGTTCCCCGCGC 533
                                                                                                                                                                                                                             Goddard A, Godowski PJ,
Pan J, Pitti RM, Roy MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                  Gurney
Smith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                   ۷, AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                  Hillan KJ;
Stone DM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disorder;
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                macrophagal, stromal and blastocoelic disorders, inflammatory, and angiogenic disorders. The polynucleotide sequences are also useful in gene therapy. ABK40254-ABK40288 encode for the human polypeptides of the invention.
                 02-JUN-1998;
02-JUN-1998;
02-JUN-1998;
03-JUN-1998;
04-JUN-1998;
05-JUN-1998;
05-JUN-1998;
05-JUN-1998;
10-JUN-1998;
11-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 569 BP; 128 A; 190 C; 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAZ65103 standard; cDNA; 570 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Membrane-bound polypeptide; PRO polypeptide; LDL receptor; pharmaceutical; receptor immunoadhesin; gene mapping; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAZ65103;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W09963088-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                  98US-0087607

98US-0087609

98US-0087759

98US-008021

98US-0088025

98US-0088029

98US-0088030

98US-0088030

98US-0088202

98US-0088202

98US-0088212

98US-0088212

98US-0088217

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98US-0088874

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98US-0088811

98US-0088824

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein PRO1245 encoding cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          99WO-US12252
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               G; 81 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 24;
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RESULT 7
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08-MAR-1999;
11-MAR-1999;
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22-JUL-1999;
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17-AUG-1999;
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18-EP-1999;
18-EP-1999;
18-EP-1999;
19-EC-1999;
01-DEC-1999;
01-DEC-1999;
01-DEC-1999;
01-DEC-1999;
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99US-140650P. 99US-144758P. 99US-144758P. 99US-146298P. 99US-149395P. 99US-151689P. 99US-151689P. 99WO-USZ1090. 99WO-USZ1090. 99WO-USZ8313. 99WO-USZ8313. 99WO-USZ8313.

Ashkenazi AJ, Marsters SA, Watanabe CK,

Pan J, Wood WI;

2002-205567/26.

AAU86141.

(GETH ) GENENTECH INC.

Claim

50; Fig 27; 302pp; English.

11-FEB-2000; 26-JUL-2001 WO200153486-A1 Homo sapiens.

2000WO-US03565

-133459P.

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Matches 78
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                                                                                                                                                                                                 The invention provides membrane-bound PRO polypeptides and polynucleotides encoding them. The PRO sequences of the invention were identified based on extracellular domain homology screening. The PRO sequences have homology with proteins including LDL receptors, TIE ligands and various enzymes. The membrane-bound proteins and receptor immunoadhesins, for instance, can be used as therapeutic agents. Receptor receptor-ligand interactions. The membrane-bound proteins can also be employed for screening of potential peptide or small molecule inhibitors of the relevant receptor-ligand interaction. The PRO encoding sequences are useful as hybridization probes, in chromosome and gene mapping and in the generation of antisense RNA and DNA. PRO nucleic acid sequences will also be useful for the preparation of PRO polypeptides, especially by recombinant techniques.
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Wood WI,
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P-PSDB;
                                                                                                                                                                         Sequence 570 BP; 129 A; 190 C; 170
                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 2; Fig 289; 822pp; English.
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DB; AAY66757.
                            534
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                                                                                                                 Similarity 100.0%;
78; Conservative
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                                                      GCGAGGACCGGGTATAAGAAGCCTCGTGGCCTTGCCCGGGCAGCCGCAGGTTCCCCGCGC
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07-JUL-1999;
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26-JUL-1999;
26-JUL-1999;
17-AIG-1999;
17-AIG-1999;
18-SEP-1999;
18-SEP-1999;
16-DEC-1999;
17-AIR-2000;
18-FEB-2000;
24-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 200 p-PSDB;
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The present invention describes human secreted and transmembrane PRO proteins. The PRO proteins have cytostatic activity. The PRO proteins can be used for targeted delivery of bloactive molecules, such as equences, and their fragments, that cause cell death. PRO nucleotide sequences, and their fragments, can be used as hybridisation probes, in chromosomal and gene mapping, and in the generation of anti-sense RMA and DNA. They may also be used to produce transgenic animals which are used to develop and screen therapeutically useful reagents. The PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zhang
                                                                                                                                                                                                                                                                                                                                  PRO polynucleotides used bioactive molecules such specific cells, to cause
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                                                                                                                                                                                                                                                                                 Claim
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DB; AAB65280.
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99WO-US28313

99WO-US28314

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                                                                                                                                                                                                                                                                                                                                         to produce polypeptides used to target as toxins, radiolabels or antibodies, targeted cell death -
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nucleotide and protein sequence can be used for tissue typing and in treating cancer. Anti-PRO antibodies can be used in diagnostic assays. C AAF44270 to AAF44470 represent PCR primers and hybridisation probes used in the isolation of human PRO sequences. AAF44087 to AAF44269 and c in the isolation of human PRO polynucleotide and protein C AAF65154 to AAF65300 represent human PRO polynucleotide and protein C sequences given in the exemplification of the present invention.
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ABX80386
ID ABX80386 standard; DNA; 570 BP.

XX
ABX80386;
AC ABX80386;
XX
DT 28-APR-2003 (first entry)
XX
DE Novel human secreted or transmembrane protein PRO1358 DNA.

Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing; cardiac insufficiency disorder; cancer; tumour; immune response; adrenal cortical capillary endothelial growth; c-fos induction; vascular endothelial growth factor inhibition; VEGF inhibition; endothelial cell growth inhibitor; T-lymphocytes stimulation; retinal neurons cell survival; rod photoreceptor cell survival; retinal disorder; retinitis pigmentosum; kidney disorder; retinitis pigmentosum; kidney disorder; remammalian kidney mesangial cell proliferation; Berger disease; dendrocyte proliferation; gene; ds. Homo sapiens.

OS Homo sapiens.

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US2002132252-Al.

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PD

19-SEP-2002.

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O5-NOV-1997; 97WO-US20069.
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16-SEP-1998; 98WO-US1947.
PR

NOT-OCT-1998; 98WO-US21141.
PR

O1-DEC-1998; 99WO-US21141.
PR

O1-DEC-1998; 99WO-US21141.
PR

O2-JUN-1999; 99WO-US0106.
PR

O3-JAN-1999; 99WO-US0106.
PR

O4-JAN-1999; 99WO-US21547.
PR

15-SEP-1999; 99WO-US21547.
PR

15-SEP-1999; 99WO-US21547.
PR

O1-DEC-1999; 99WO-US28301.
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98US-08532P

98US-08802P

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98US-08931P

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                                Human secreted/transmembrane protein cDNA, #163
                                                                 22-APR-2003 (first entry)
Human; gene; ss; PRO; secreted; transmembrane; pharmaceutical;
                                                                                                 ABX80890;
                                                                                                                                   ABX80890 standard; cDNA; 570
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P-PSDB; ABU59174.
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100.0%; Pred. No. 1.1
cive 0; Mismatches
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DB 25; I . 1.5e-06; ches 0;

Length 570 Indels

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Gaps

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The invention describes an isolated human PRO polypeptide. The PRO CC polypeptides are useful in detecting PRO polypeptides in a sample, in CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and CC in modulating at least one biological activity of a cell expressing a PRO CC useful for treating cardiac insufficiency disorders. PRO1312 stimulates hypertrophy of neonatal heart and is thus CC useful for treating cardiac insufficiency disorders. PRO1186 and PRO1387 induce c-fos in endothelial growth, and PRO536, CC PRO1450 and PRO1387 induce c-fos in endothelial growth, and PRO536, CC PRO1560 and PRO1387 induce c-fos in endothelial growth, and PRO536, CC PRO1560 and PRO1387 induce c-fos in endothelial cells, and are thus cells are thus useful for treating conditions or disorders where angiogenesis would be beneficial, e.g. wound healing and anaagonist of this polypeptide are useful for treating cancerous tumours. PRO812 inhibits vascular cells and is thus useful for inhibiting endothelial cell growth in CC pRO1068, PRO1184, PRO1346 and PRO1375 stimulated proliferation of endothelial cell growth in PRO826, PRO1068, PRO1184, PRO1346 and PRO1375 stimulated proliferation of commune response. PRO828, PRO826, PRO1068 proliferation of growth provides and are therapeutically useful for treating cells; and therefore are useful for treating retinal cell disorders of injuries, e.g. retinitis plamentosum, AMD. PRO813, PRO813, PRO183 and therefore are useful for treating kidney disorders associated with demartitis, herpetiformis or Crohn's cells associated with dermartitis, herpetiformis or Crohn's cells are thus useful for treating sports injuries, and arthritis. This cequence represents a novel human PRO protein polynucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Zhang Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 2; Fig 291; 648pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346 and PRO1375, which stimulate proliferation of stimulated T-lymphocytes are therapeutically useful for enhancing immune response and in cancer are therapeutically useful for enhancing immune response and in cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Paoni
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| אם ש<br>אם אמים<br>אמים<br>אמים<br>אמים<br>אמים<br>אמים<br>אמים<br>אמים                                                      | אק ק<br>א א ק<br>א א א ק<br>א א א ק ק                                                                                                         | א א א א א א א א א א א א א א א א א א א                                                                                                                                            | קק<br>אקט קק קק<br>אק אק קקק<br>אק אקקק                                                                                                                                                                       | ק<br>ק<br>ק<br>ק<br>ק<br>ק<br>ק<br>ק<br>ק<br>ק<br>ק<br>ק<br>ק<br>ק<br>ק<br>ק<br>ק<br>ק<br>ק                                                                                                                                                                                                                                                                                                                                        | אק ק<br>אק<br>אק קק<br>אקק<br>אקק<br>אקק<br>אקק<br>אקק                                                                                                                                       | רק<br>אק<br>אק<br>אק<br>אק<br>אק<br>אק<br>אק<br>אק<br>אק                                                                          |
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                                                                                               human
     PRO; hypertrophy of neonatal heart; angiogenesis; wound he insufficiency disorder; cancer; tumour; immune response; cortical capillary endothelial growth; c-fos induction; ar endothelial growth factor inhibition; VEGF inhibition;
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L Similarity 100.0%;
78; Conservative (
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                                                                                                                                                                                                  standard;
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                                                                                                                                                                                                  DNA;
                                                                                             Or.
                                                                                             transmembrane
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                                                                                                                                                                                                  ВP
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                                                                                           protein PRO1358
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1.5e-06;
hes 0;
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98WO-US19437.
98WO-US19437.
98WO-US19437.
98WO-US21141.
98WO-US21141.
98WO-US25106.
99WO-US25109.
99WO-US2526.
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AC ABX90
XX 01-MA
XX U1-MA
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XX Human
XX Pharm
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XX Homo
OS Homo
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04-AUG-1998;

10-AUG-1998;

10-AUG-1998;

11-AUG-1998;

11
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pharmaceutical; 
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98WO-US1930

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2000WO-US26331

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2000WO-US27377

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                                                                                                                                                                                                                               В
                                                                                         Qy
                                                                                                                                                                                                                                                      The invention discloses isolated PRO secreted/transmembrane polypeptides CC comprising a sequence without signal peptide and the nucleic acid CC encoding them. The polypeptides can be used to raise antibodies that CC specifically bind to the PRO polypeptide, for linking a bloactive molecule to a cell expressing a PRO protein and for modulating at least CC one biological activity of a cell. The PRO polypeptides or polynucleotides are also useful in gene therapy, in chromosome CC identification, as chromosome markers, or in generating probes. The PRO CC polypeptides are useful as molecular markers for protein CC electrophoresis, and the isolated nucleic acids may be used for CC electrophoresis, and the isolated nucleic acids may be used for CC acids may also be used in tissue typing. Anti-PRO antibodies are useful in diagnostic assays for PRO, and in affinity purification of PRO from CC acids may also be used in tissue typing. Anti-PRO antibodies are useful CC in diagnostic assays for PRO, and in affinity purification of PRO from CC ADX90083-ABX90468 are the genes encoding, the primers amplifying and the CC Note: The sequence data for this patent is also available in electronic CC format from USPTO at sequence supports.
                                                                                                                                      Query Match
Best Local S
Matches 78
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10-JUN-1998;
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11-JUN-1998;
                                                                                                                                                                                                                               Sequence 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 2; Fig 289; 650pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New transmembrane polypeptides and nucleic acids encoding the polypeptides, useful in gene therapy, in chromosome identification, chromosome markers, or in generating probes .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Zhang Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-288106/28.
P-PSDB; ABU60604.
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                                                                                                                               ch 14.2%; Score 78; DB 25; I
1 Similarity 100.0%; Pred. No. 1.5e-06;
78; Conservative 0; Mismatches 0;
                                           GCGAGGACCGGGTATAAGAAGCCTCGTGGCCTTGCCCGGGCAGCCGCAGGTTCCCCGCGC
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|                                                                                                                                                    |                                                                                                                                                                                                                                                                            |                                                                                                                                                                                                                                          | _                                                                                                                                               |                                                                                                                                                  |                                                                                        |
| יי<br>אר<br>אר<br>אר<br>אר<br>אר<br>אר<br>אר<br>אר<br>אר<br>אר<br>אר<br>אר<br>אר                                                                   | יי<br>קיק<br>קיק<br>קיק<br>קיק<br>קיק<br>קיק<br>קיק<br>קיק<br>קיק                                                                                                                                                                                                          | קי<br>אס א<br>אס א אס אס אס אס אס אס אס אס אס אס אס אס                                                                                                                                                                                   |                                                                                                                                                 |                                                                                                                                                  |                                                                                        |
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0; Mismatches 0;
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17-JUN-1998; 98US-08950P.
18-JUN-1998; 98US-08990P.
28-AUG-2001; 2001US-09411992.
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(GETH ) GENENTECH INC.

Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL; Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ; Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF; Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI; Zhang Z;

WPI; 2003-155950/15. P-PSDB; ABU59026.

New secreted and transmembrane PRO polypeptides (e.g. PRO183, PRO184, PRO361 or PRO846) useful as targets for therapeutic intervention in cancers (e.g. lung or breast cancers), or for diagnosing these cancers

Claim 2; Fig 289; 647pp; English.

The invention discloses isolated PRO secreted/transmembrane polypeptides comprising a sequence without signal peptide and the nucleic acid encoding them. The polypeptides can be used to raise antibodies that specifically bind to the PRO polypeptide, for linking a bioactive molecule to a cell expressing a PRO protein and for modulating at least one biological activity of a cell. The PRO polypeptides or polynucleotides are also useful as pharmaceuticals, diagnostics, polynucleotides are also useful as pharmaceuticals, diagnostics, mammalls, e.g. humans, dogs, catts, cattle, horses, sheep, pigs, goats or rabbits as targets for therapeutic intervention in certain cancers (e.g. colon, lung or breast cancers) and diagnostic determination of the presence of these cancers. The PRO polypeptides are also useful as molecular weight markers or for chromosome identification. The PRO genes

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                                                                                                                                                                               invention. Note: The
                                                                                                                                           Sequence
                                            534 GCCCCGAGCCCCCGCGCC
                                                                                                                                                                 The sequence data for this patent is also available in electronic t from USPTO at seqdata.uspto.gov/sequence.html.
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Direct Submission

Submitted (02-yUN-1999) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila
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Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.

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BX415111 Homo sapiens THYMUS
5-PRIME, mRNA sequence.
BX415111
BX415111
GI:30765470
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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145; Conser
                                                                                            CNS015Y4 1203 bp DNA linear GSS 26-JUL-1999 Drosophila melanogaster genome survey sequence T7 end of BAC BACN15El0 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.
AL106054
AL106054.1 GI:5619805
Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                  SSD
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BP 191 9106 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact: Feng Liang Email: fliangelifetech.com
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSOCAP004BE10QP1.
Location/Qualifiers
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/clone="CSOCAPO04Y120"
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/clone=1lb="Homo sapiens THYMUS"
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Library was not normalized."
257 c 323 g 18 t 207 others
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Pred. No. 1.5e-05;
7; Mismatches 202;
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175; Conserv
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Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
        AG032885
Pan troglodytes DNA,
AG032885
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1 (bases 1 to 1203)
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/clone="BACN15E10"
/clone="BACN15E10"
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/note="end : T?"
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Unpublished | 2 (bases 1...
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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                                       GCCGCAGCAGGAAGTTGGCCAGGGCACGGCAGCGTGAGCGGAGCGGCAGGGCTTTCTCAGG 446
                                                                                                            CAAGAGGAAGTCCTCGAGGCCCGGGCAGGGAAGGGGGCACGGCCTTCCCAGGGCCCGCCG
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    CGGNCGGCGGNGCGGCGNGCGGNCGGCGNGCGCACACGGCGNGGGAAGGCCGG
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R.Site 1 : SacI
R.Site 2 : SacI.
Location/Qualifiers
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389 c 502 g 132 t 2
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/mol_type="genomic DNA"
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/clone="PTB-007M05.F"
/sex="mmale"
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Pred. No. 6.6e-05;
0; Mismatches 296;
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AL Submitted (02-7UN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfily.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain 92; on bw sp. the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be Location/Qualifiers

Location/Qualifiers

lice

1. 925 The BDGP ST Library of the BDGP Center can be constructed by the same strain become the same strain become the same strain become the library of the same strain become the library of the same strain become the library of the same strain become the library of the same strain become the library of the same strain become the library of the same strain become the library of the same strain become the library of the same strain become the library of the same strain become the library of the same strain become the library of the same strain become the same strain become the library of the same strain become the same strain become the library of the same strain become the same strain become the same strain become the same strain become the same strain become the same strain become the same strain become the same strain become the same strain become the same strain become strain become strain become the same strain become st
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Direct Submission
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TGCCTCTCAGAGGGCCCCAGCGCCTGCCAAGAGGAAGTCCTCGAGGCCCGGGCAGGGA
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/note="end: TET3"
61 c 61 g 172 t 511 c
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Pred. No. 7.8e-05;
5; Mismatches 128;
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  survey sequence TET3 end of BAC #
rom Drosophila melanogaster (fruit
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Duke University
Durham, NC 27708-1000
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1281 bp mRNA linear EST 29-MAY-201
1024034A03.y2 C. reinhardtii CC-1690, normalized, Lambda Zap II
Chlamydomonas reinhardtii cDNA, mRNA sequence.
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BG852363.1 GI:14233547
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                                                                                                                            Conservative
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/organism="Chlamydomonas reinhardtii"
/mol_type="mRNA"
/mol_type="mRNA"
/strain="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
/clone_lib="C. reinhardtii CC-1690, normalized, Lambda Zap
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Butte (1992) Divisional de Sequence was carried out as part of a collaboration with the Berkeley Drosophila Decephila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the 1809enic strain y2; on bw sp. the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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survey sequence T7 end of BAC #
rom Drosophila melanogaster (fruit
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649

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163; Conserv
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Fujiyama, A., Hattori, M., Toyoda, A., Tay
Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama,
and Chemical Research (RIKEN), Genomic
                                                                                                               Pan troglodytes (chimpanzee)
Pan troglodytes
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                   AG043499 949 bp DNA
Pan troglodytes DNA, clone: PTB-021N08
AG043499
                                                              BAC end sequences of Library Unpublished
                                                                                               Fujiyama,A.,
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/clone="lb-"Rpc1-98"
/note="end : T7"
5 a 202 c 241 g 91 t 243 of
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                                                                                     Watanabe,
                                                                                               Hattori, M.,
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and Sakaki, Y.
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BQ681076 bp
AGENCOURT_8187867 NIH_MGC_112 Homo
5', mRNA sequence.
BQ681076 BC681076.1 GI:21793755
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1-7-22 Suehiro-chou Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:hhttp://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170) Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of netwers.
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R.Site 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="raxon:9598"
/clone="PTB-021N08.F"
/sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
/ 465 c 281 g 35 t 113 others
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| QΥ 304 CACG                          |             | Qy 422 GCGGAGCGGCAGGCTTTCTCAGGAGCGCGGGGGGAGGCCGCGCTGGAGGGCGGAGGAC 481                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
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| Qy 246 GCAA                          |             | 0                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| Db 695 ASCA                          |             | Qy         242 GACCGCAAAGCGAAGGTGCGGGCCGGGGTGGGCCTCGCGCGAGAGACAAAGCGAAGCGGCCTGCC         301           Db         660 GGCGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
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| Oy 126 ACCA                          |             |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
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| Query Match<br>Best Local Simila     |             |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| ORIGIN                               |             | pb 840 GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |
| BASE COUNT 254                       |             | QY 62 GCAGAAGGCGCCACGAGGACCCCCCAGTGCCCGACGTTGCCACGGGTTCGGGATCAGAGGC 121                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
|                                      |             | Db 900 GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
|                                      |             | င္ပ                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |
|                                      |             | Best Local Similarity 45.6%; Pred. No. 0.00036; Matches 250; Conservative 0; Mismatches 296; Indels 2; Gaps 1;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| FEATURES<br>source                   | <u> </u>    | y Match 13.4%;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| project<br>and Gen<br>pBeloba        |             | NIH_MGC Library."  BASE COUNT 63 a 593 c 314 g 55 t 40 others ORIGIN                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
| library<br>d'Etude                   |             | Berkeley) using ZAP-cDNA synthesis kit (stratagene) and Superscript II RT (Life Technologies). Note: this is a                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
|                                      |             | GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
| COMMENT Determi                      |             | into EcoRI/XhoI sites using the following 5' adaptor:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
| AL                                   |             | /clone_ilp="Nih_woc_ilic" /note="organ: ship; Vector: poTB7; Site_1: XhoI; Site_2: /note="organ: ship; Vector: poTB7; Site_1: XhoI; Site_2:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
| AUTHORS Genosco                      |             | /Labaue_type "canton of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the pla |
|                                      |             | /clone="IMAGE:6259803" /rissue type="melanotic melanoma, cell line"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |
| Neopter<br>Neopter                   | <del></del> | /mol_type="mRNA" /dh xref="taxon:9606"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| MSIN                                 |             | rce                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |
| S                                    |             | FEATURES Location/Qualifiers                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
| ACCESSION AL10846<br>VERSION AL10846 |             | http://image.lini.gov<br>Plate: LLCM417 row: o column: 04                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
| BACN37Li<br>fly), go                 |             | Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| 4                                    |             | CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
| RESULT 11                            |             | Email: Cgapps-remail: http://grv<br>Tissue Procurement: DCTD/DTP                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
| Db 362 GGCGGC                        |             | AL Unpublished Contact: Robert Strausberg, Ph                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
| Qy 542 cccccc                        |             | Nat                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |
| pb 422 ggggg                         | _           | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE 1 (bases 1 to 1065)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |
| Qy 482 CGGGTA                        |             | NISM Homo                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
| Db 482 CCGGCC                        |             | SOURCE Homo sapiens (human)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |

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75Y
2010 phila melanogaster genome survey sequence SP6 end of BAC 11.08 of DrosBAC library from DrosSophila melanogaster (fruit genomic survey sequence.
260 160.1 GI:5628764
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3GGCG 355
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phila melanogaster
yota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
era; Endopterygota; Diptera; Brachycera; Muscomorpha;
coidea; Drosophilidae; Drosophila.
                                                                                                        TATAAGAAGCCTCGTGGCCTTGCCCGGGCAGCCGCAGGTTCCCCGCGCGCCCCGAG
GGGCTTCCCAGGGCCGGCCGGCCGCAGCAGGAAGTTGGCCAGGCCAGGCCGTGAGC 423
                                                                                                                                                                   CGGSAGCGGRRKGCAACKSAGMSSCGGRSGSGGSSCCGGKKAKGGVRGGRVCCAGGG 694
                                                                                                                                                                                                                                                          AGGGAGCCAGGAACTGCGCCGCCCCCGCCCCTGCCCTGGCGCGAGGGAAGCTCCCTC 185
                                                                                                                                                                                                                                                                                        13.4%; Score 73.6; DB 29; larity 16.1%; Pred. No. 0.00036; Conservative 207; Mismatches 146;
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                                                                          GAGGGCCCCAGCGCCT--GCCAAGAGGAAGTCCTCGAGGCCCGGGCAGGGAAGGGGG 363
                                                                                                                                                                                                                                                                                                                                                             /organism="Drosophila melanogaster"
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1 a 176 c 160 g 152 t 359 otl
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Matches 256;
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BG786331/c
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                                                           127
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                                                                              67 AGGCGCCCACGAGGACCCCCAGTGCCCGACGTTGCCACGGTCTGGGATCAGAGGCAGGGA 126
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                                                                                                                                                                                                Similarity 47.3
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4400 Fifth Avenue, Pittsburgh, P
Tel: +1 412 268 5849
Email: ettensohn@andrew.cmu.edu.
Location/Qualifiers
1. .1040
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BG786331
BG786331.1
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Dept. Biol. Sci.
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Strongylocentrotus purpuratus
Eukaryota, Metazoa, Echinodermata, Eleutherozoa, Echinozoa,
Echinoidea, Euechinoidea, Echinocea, Echinoida,
Strongylocentrotidae, Strongylocentrotus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BG786331 1040 bp mRNA linear EST 20-MAY-2001
SEAUMC006288 Sea urchin primary mesenchyme cell cDNA library
Strongylocentrotus purpuratus cDNA clone PC_0028_A2_G12_MR 5', mRNA
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           GGGAGGCGGCCGGGAGTGAGCCTGATCGTCCCTGGCGCCTCCACCTCCCAGGCGCAGA 66
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,X., Mahairas,G., Illies,M.R., Cameron,R.A., Davidson,E.H. and
                                                                                                                                                                                                                                                                                    20
                                                                                                                                                                                                                                                             library"
//note="Vector: pSPORT1; Site_1: Not1; Site_2: Sal1;
dt priming from poly A+ RNA, directionally cloned"
a 499 c 472 g 44 t 5 others
                                                                                                                                                                                                                                                                                                                                                             /organism="Strongylocentrotus purpura
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                                                                                                                                                                                                                 13.38;
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Pred. No. 0.00042;
0; Mismatches 285;
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                                                                                                                                                                                                               Genoscope Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 10245.r
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.gei7seg-C908G006BD03NP1&cluster=10245.r. Containtp://gulltength.invitrogen.com/ InvitroGen Corporation 1600
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraddy Avenue Genoscope sequence ID : CSOAG006BD03NP1.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Verto
Mammalia; Eutheria; Primates; Catarrhini; Hon
1 (bases 1 to 1201)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
Contact: Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BX405071 1201 bp mRNA linear i BX405071 Homo sapiens B CELLS (RAMOS CELL LINE) Homo clone CSODG006YG06 3-PRIME, mRNA sequence.
BX405071 BX405071.1 GI:30648111 EST.
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/note="Wector: pcMVSPORT_6; 1st strand CDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand CDNA was digested with Not I and EcoRV sites of the pcMVSPORT 6 vector.
Library was not normalized."
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                                                                                                                                                                                                              sequence.
AG152796
AG152796.1 GI:16682474
GSS.
Pan troglodytes (chimpanzee)
Pan troglodytes
Eukaryota; Metazoa; Chordata; C
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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6; Conservative
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5', mRNA sequence.
BU502934 BU502934.1 GI:22808397
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Clones are derived from the chimpanzee BAC library RPCI-43 This end was generated during the R&D process and may have higher chapter characteristic errors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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/mol_type="genomic DNA"
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/clone="rp43-016F02.TJ"
/csex="male"
/csex="male"
/cell_type="lymphocytes"
/cell_type="lymphocytes"
/clone_lib="rPCI-43 Chimpanzee Male BAC L:
445 c 468 g 31 t 96 others
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                        (house mouse)
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Mus
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J.0006;
277;
                                                                                                musculus
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Indels Length 1085;

0;

Gaps

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60

Library"

CDNA

linear | DNA clone

EST 12-SEP-2002 E IMAGE:6489733

480

420 932

992

360 872 300 812 240 752

| • | 483 GGG<br>                                       | 783 CGC<br>423 CGG<br>11<br>723 GGG                  | 04<br>43<br>64                                                 | 963 CGC<br>249 AAG<br>1<br>903 GGG     | 89                                                        | 71 GCC<br>  <br>1083 GCG                                    | 11 GGC<br>                                                   | Query Match<br>Best Local Simi<br>Matches 265;                                                                            | SOUICE BASE COUNT ORIGIN                                                                                        | ***** HI                                                                                                                                                                                                                                                                                                                                                         | REFERENCE 1 (base<br>RAUTHORS NIH-MGC<br>TITLE NATIONAL<br>JOURNAL Unpublis<br>COMMENT CONTACT:<br>Email: C                                                                                        |
|---|---------------------------------------------------|------------------------------------------------------|----------------------------------------------------------------|----------------------------------------|-----------------------------------------------------------|-------------------------------------------------------------|--------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| _ | GGGTATAAGAAGCTTCGTGGCGGGGGCAGCCGCAGGTTCCCCGCGCGCG | CCCCCCCGCCGCCGCCGCCCCCCCCCCCCCCCCCCCCC               | TCTCAGAGGGCCCCAGCGCCAGCGAAGGGAAGTCCTCGAGGCCCGGGCAGGGAAGGGGGGGG | CÓCCGCGGGGGGCGCGCGGGGGGGGGGGGGGGGGGGGG | AGGGAGCAGGAACTGCGCCCCCGCCCCCTGCCCTGGCGCGAGGGAAGCTCCCTCACC | GCCCACGAGGACCCCCAGTGCCCGACGTTGCCACCGGTCTGGGATCAGAGGCAGGGACC | GGCGGCCGGGAGTGAGGCCTGATCGTCCGCGGCGCCTCCACCTCCCCAGGCGCAGAAGGC | 13.1%; Score 72.2; DB 13; Length 114<br>Similarity 48.3%; Pred. No. 0.00065;<br>5; Conservative 0; Mismatches 276; Indels | resistant)" r: pCMV-SPORT6; Sit directionally; olig directional by Life constructed by Life Library." 61 others | Procurement: The Cepko Laboratory Library Preparation: Life Technologies, Inc. Library Arrayed by: The I.M.A.G.E. Consortium squencing by: Agencourt Bioscience Corporation distribution: MGC clone distribution informat through the I.M.A.G.E. Consortium/LLNL at: //image.llhl.gov LLAM14038 row: g column: 14 Lality sequence stop: 353. Location/Qualifiers | ; Eutheria; Rodentia; Sciurognathi; Muridae; \$ 1 to 1143) \$ 1 to 1143) http://mgc.nci.nih.gov/. Institutes of Health, Mammalian Gene Collected hed Robert Strausberg, Ph.D. Gabbs-remail.nih.gov |
|   | GCCCCGAGC 542                                     | GCCGGCGCG 724 GCGAGGACC 482           CGGGGGGGCG 664 | 4 7 3                                                          | ceeececc 904 secrecerc 303             | N 9 H                                                     | AGGGACC 128<br>    <br>GGCCGGCGN 102                        | GCAGAAGGC 70<br>     <br>  GCGCGGGG 1084                     | 3;<br>8; Gaps 3                                                                                                           | e_1: NotI;<br>io-dT primed.<br>id for<br>Technologies.                                                          | (LLNL)                                                                                                                                                                                                                                                                                                                                                           | Murinae, Mus.                                                                                                                                                                                      |

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